```
                    GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on:      April 5, 2006, 21:01:08 ; Search time 235 Seconds
                                        (without alignments)
                                     8063.322 Million cell updates/sec

Title:          US-10-757-356-17
Perfect score:  1066
Sequence:       1 attcgccctggtgattgga.........atcgaagccgaaaaaaaa 1066

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters:      2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_NA:*
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             2: /cgn2_6/ptcdata/1/ina/5_COMB.seq:*
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             5: /cgn2_6/ptcdata/1/ina/H_COMB.seq:*
             6: /cgn2_6/ptcdata/1/ina/PCTUS_COMB.seq:*
             7: /cgn2_6/ptcdata/1/ina/PP_COMB.seq:*
             8: /cgn2_6/ptcdata/1/ina/RE_COMB.seq:*
             9: /cgn2_6/ptcdata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	517.2	48.5	860	3	US-10-244-779-1	Sequence 1, Appli
2	419.6	39.4	801	3	US-09-459-956-7	Sequence 7, Appli
3	256.6	24.1	678	3	US-09-459-956-6	Sequence 6, Appli
4	256.6	24.1	859	3	US-09-866-538-11	Sequence 11, Appl
5	256.6	24.1	859	3	US-09-865-291-11	Sequence 11, Appl
6	237.2	22.3	699	3	US-09-459-956-5	Sequence 5, Appli
7	222.4	20.9	723	3	US-10-152-296-1	Sequence 1, Appli
8	219.8	20.6	6984	3	US-10-001-189-45	Sequence 45, Appl
9	208	19.5	690	3	US-09-459-956-2	Sequence 2, Appli
10	177.8	16.7	696	3	US-09-459-956-4	Sequence 4, Appli
11	176.2	16.5	696	3	US-09-459-956-3	Sequence 3, Appli
12	139.2	13.1	1482	3	US-09-977-897-1	Sequence 1, Appli
13	132.2	12.4	720	3	US-10-021-818A-1	Sequence 1, Appli
14	126	11.8	720	3	US-09-839-650-1	Sequence 1, Appli
15	126	11.8	720	3	US-10-652-703A-1	Sequence 1, Appli
16	126	11.8	720	3	US-10-021-818A-3	Sequence 3, Appli
17	126	11.8	1079	3	US-09-609-161B-15	Sequence 15, Appl
18	126	11.8	1079	3	US-09-626-581D-64	Sequence 64, Appl
19	126	11.8	1079	3	US-09-415-765B-64	Sequence 64, Appl
20	126	11.8	1079	3	US-09-626-580C-64	Sequence 64, Appl
21	126	11.8	1085	3	US-09-277-716-15	Sequence 15, Appl
22	122.8	11.5	1021	3	US-09-839-650-2	Sequence 2, Appli
23	122.8	11.5	1021	3	US-10-652-703A-2	Sequence 2, Appli
24	118.8	11.1	1104	3	US-09-277-716-30	Sequence 30, Appl
25	118.8	11.1	1104	3	US-09-609-161B-30	Sequence 30, Appl
26	118	11.1	1279	3	US-09-277-716-31	Sequence 31, Appl
27	118	11.1	1279	3	US-09-609-161B-31	Sequence 31, Appl
c 28	45.6	4.3	7218	3	US-08-232-463-14	Sequence 14, Appl
29	45.4	4.3	720	3	US-09-172-063-14	Sequence 14, Appl
30	45.4	4.3	720	3	US-09-316-919-15	Sequence 15, Appl
31	45.4	4.3	720	3	US-09-602-641-14	Sequence 14, Appl
32	45.4	4.3	720	3	US-09-316-920A-15	Sequence 15, Appl
33	45.4	4.3	720	3	US-09-866-538-9	Sequence 9, Appli
34	45.4	4.3	720	3	US-09-865-291-9	Sequence 9, Appli
35	44.8	4.2	3171	3	US-09-513-783A-31	Sequence 31, Appl
36	44.8	4.2	3171	3	US-09-430-656-31	Sequence 31, Appl
37	44.8	4.2	3171	3	US-10-100-957A-31	Sequence 31, Appl
38	44.2	4.1	4944	3	US-10-001-189-56	Sequence 56, Appl
39	44.2	4.1	4951	3	US-10-001-189-51	Sequence 51, Appl
40	44.2	4.1	8999	3	US-10-001-189-48	Sequence 48, Appl
41	44	4.1	972	3	US-09-172-063-30	Sequence 30, Appl
42	44	4.1	972	3	US-09-602-641-30	Sequence 30, Appl
43	43.8	4.1	717	3	US-09-513-783A-43	Sequence 43, Appl
44	43.8	4.1	717	3	US-09-430-656-43	Sequence 43, Appl
45	43.8	4.1	717	3	US-10-100-957A-43	Sequence 43, Appl

ALIGNMENTS

```
RESULT 1
US-10-244-779-1
; Sequence 1, Application US/1024779
; Patent No. 6933375
; GENERAL INFORMATION:
; APPLICANT: Falkowski, Paul
; APPLICANT: Sun, Yi
; APPLICANT: Gorbunov, Maxim
; APPLICANT: Wyman, Kevin
; APPLICANT: Chen, Yi-Bu
; TITLE OF INVENTION: mcPP Encoding Nucleic Acids,
; TITLE OF INVENTION: Polypeptides, Antibodies and Methods of Use Thereof
; FILE REFERENCE: Rut 00-0023US
; CURRENT APPLICATION NUMBER: US/10/244,779
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: 60/322,189
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 860
; TYPE: DNA
; ORGANISM: Montastrea cavernosa
US-10-244-779-1

  Query Match       48.5%;   Score 517.2;   DB 3;   Length 860;
  Best Local Similarity   80.5%;   Pred. No. 8.6e-160;
  Matches  668;   Conservative   0;   Mismatches 128;   Indels  34;   Gaps   4;

Qy    1 ATTCGCCCTGGTGATTGGAAGAGAGAGCAGAGTCGAGAACAACAAGAGCTGTAAGGTTGATA 60
          ||||||||||||||| |||| |||||||||||||||||
Db   54 ATTCACCCTGGTGATTGGAAGCGAGCGCAAATCTAGAAGAACAAGCGGCTGTAAGACTGATA 113

Qy   61 TCTTAC-TTAGTCTACCATCATGACAAGTGTTGCACAGGAAAAGGGTGTGATTAAACCA 119
          ||||   |||||||| |||||||  || || || |||||||| |||
Db  114 TCTTACTTTACGTCTACCATCATGA----------GTGTGATTAAATCA 152

Qy  120 GACATGAAGATGAAGCTGCGTATGGAAGGTGCTGTAAACGGCACAAGTTCGTGGTTGAA 179
          |||||||| ||| |||||||||||||||||||  |||||||||| |||
Db  153 GTCATGAAAATCAAGTGCGTATGGACGGCATTGTAAACGGGCACAAGTTCATGATTACA 212

Qy  180 GGAGATGGAAAAGGGAAGCCTTTCGACGGAACAACAGACTATGGACCTTACAGTCATAGAA 239
          |||||||||||||| |||||||||||||||  ||||
Db  213 GGAGAGGTGAAGGCAAGCGCCTTTCGAGGGAACACACCACTATAATACTTAAAGTCAAAGAA 272

Qy  240 GGCGCACCATTGCCTTTCGCTTACGATATCTTGACAACAGTATTCGATTACGCGCCACAGG 299
          |||| |||| |  |||||||||  |||||||||||||||||||| |||||||
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Db   112 TTAAACCAGACATGAAGATGAAGCTGCGTATGGAAGGTGCTGTAAACGGGCACAGTTCG 171
         |||||||||||||||||||  || |  || |  ||||| ||| |  ||  || |||| |
Qy   137 TTAAACCAGACATGAAGAGATTAAGCTGAAGATGAAGGGAAGCATGCATGGGCACAGTTTG 196

Db   172 TGGTTGAACGGAGATGGAAAAGGGAAGCCTTTCGACGGACCAGACATGCGACCTTACAG 231
         || |||| ||| |  ||| |  | |||||  |||||  | || || || | |  |||| |
Qy   197 TGATCGAAGGAGAGGAGGAGGAGAAGCCTTACGATGGGACACACACTTTAAACCTGGAAG 256

Db   232 TCATAGAAGGCGCCACCATTGCCTTTCGCTTACTAGGCCGTTGACAACAGTATTCGATTACG 291
         | | || ||  |  ||| || || | | ||  | ||  | |||  ||||  || |  ||||
Qy   257 TGAAGGAAGTGCGGCCTCGCCGCCTTTTCTTACGATATCTTGTCAAACGCGGTTCCAGTACG 316

Qy   292 GCAACAGGGTATTCGCCAAATACCCAGAAGACATAGCAGATTATTCAAGCAGACGTTTC 351
         | || || |  ||  | || ||| ||||| || || || || |||||| || | ||||
Db   317 GAAACAGAGCATTGACAAAATACCCAGAAGACGATATAGCAGCTATTTCAAGCAGCGTGTTTC 376

Qy   352 CTGAGGGGTACTTCTGGAACGAGCATGACATGACATCGAAGACCAGCAGGGCATTGCATCGCCA 411
         |  ||||| | ||  |||  |||||||  ||| | | |||| |   ||||  ||| || ||  |
Db   377 CCGAGGGATATTCCTGGAAAGAACCATGACTTTGAAGACAAAGGCATTGTCAAAGTGA 436

Qy   412 CAAACGACATAACAATGATGGAAGGCGTCGACGACTGTTTTGCCTATAAAATTCGATTTG 471
         | ||  || |  | || ||||| | |    |||       |  ||| | | ||| ||| |
Db   437 AAAGTGACATAAGCATGACGAGGAA------GACTCCTTATCTATCATGAAATTCGTTTTG 487

Qy   472 ATGGTGTGAACTTTCCTGCCAATGTCCAGTTATGCAGAGGAAGACGCTGAAATGGGAGC 531
         |||  || |||||||||  || |||||| | |||| |||||| |||  || |  |||  |
Db   488 ATGGGATGAACTTTCCTCCCAATGTCCGGTTATGCAGAAAAAAACTTTGAAGTGGGAAC 547

Qy   532 CATCCACTGAGATAATGTATGCGCGTGCGTGATGGAGGGTGATGTTAACATGGCTC 591
         |||||| |||| | |||| |  |  |||  ||| |||  || |||| |||  ||| |
Db   548 CATCCACTGAGATATGCATTATGTACGTGCGTGGTCGGGAGATATTAGCCATTCTC 607

Qy   592 TGTTGCTTGAAGGAGGTGGCCATTACCGATGTGACTTCAAAACTACTTACCAAAGTAAGA 651
         ||||| ||||||  |||| || |||| |  || ||||  ||| ||| |  ||| || ||
Db   608 TGTTGCTCGGAGGAGGTGGCCATTACCGATGTGACTTCAAAAGTATTTACAAAGCAAAA 667

Qy   652 AGGTTGTCCGTTGCCAGACTATCACTTTGTGCACGAGCATGCCGAAGCTCGTCAT 711
         ||  || |  || ||||| | |||| |||| || | | || | |||| |  ||||
Db   668 AAGTTGTCAAATTGCCAGACTATCACTTTGTGCACGATGAGAATGCAGTTGCTCGCTAT 727

Qy   712 ACAAAGATTACAACAAGGTTAAGCTGCACGAGCATGCCGAAGCTCGTCAT 761
         ||||||||||||||  ||| |||||  |||| |  || | |||  ||| |
Db   728 ACAAGGATTACAACAAAGTTAACGCGTGTATGAGAATGCAGTTGCTCGCTAT 777
```

RESULT 2
US-09-459-956-7
; Sequence 7, Application US/09459956
; Patent No. 6342379
; GENERAL INFORMATION:
;   APPLICANT: Tsien, Roger Y.
;   APPLICANT: Gonzalez, III, Jesus E.
;   TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY
;   TITLE OF INVENTION: OPTICAL METHODS
;   FILE REFERENCE: REGEN1290-4
;   CURRENT APPLICATION NUMBER: US/09/459,956
;   CURRENT FILING DATE: 1999-12-13
;   PRIOR APPLICATION NUMBER: 08/765,860
;   PRIOR FILING DATE: 1999-05-08
;   PRIOR APPLICATION NUMBER: 08/481,977
;   PRIOR FILING DATE: 1995-06-07
;   PRIOR APPLICATION NUMBER: PCT/US96/09652
;   PRIOR FILING DATE: 1996-06-06
;   NUMBER OF SEQ ID NOS: 22
;   SOFTWARE: FastSEQ for Windows Version 4.0
;   SEQ ID NO 7
;   LENGTH: 801
;   TYPE: DNA
;   ORGANISM: Clavularia sp
US-09-459-956-7

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Query Match        39.4%;  Score 419.6;  DB 3;  Length 801;
Best Local Similarity 75.6%;  Pred. No. 1.3e-127;
Matches 537;  Conservative 0;  Mismatches 164;  Indels 9;  Gaps 1;

Qy    52 AGGTTGATATCTTACTTACGTCTCCACCATCATGACAAGTGTTGCACAGGAAAAGGGTGTGA 111
         |||  |  | ||| ||| |  |  ||| ||| |||| | | | || ||||||| ||||||||
Db    77 AGGCTGACTTAGAAGAGAAGACACATTGAGAATTACCAACAACTCTAACCACCACGGTGTGA 136
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RESULT 3
US-09-459-956-6
; Sequence 6, Application US/09459956
; Patent No. 6342379
; GENERAL INFORMATION:
;   APPLICANT: Tsien, Roger Y.
;   APPLICANT: Gonzalez, III, Jesus E.
;   TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY
;   TITLE OF INVENTION: OPTICAL METHODS
;   FILE REFERENCE: REGEN1290-4
;   CURRENT APPLICATION NUMBER: US/09/459,956
;   CURRENT FILING DATE: 1999-12-13
;   PRIOR APPLICATION NUMBER: 08/765,860
;   PRIOR FILING DATE: 1999-05-08
;   PRIOR APPLICATION NUMBER: 08/481,977
;   PRIOR FILING DATE: 1995-06-07
;   PRIOR APPLICATION NUMBER: PCT/US96/09652
;   PRIOR FILING DATE: 1996-06-06
;   NUMBER OF SEQ ID NOS: 22
;   SOFTWARE: FastSEQ for Windows Version 4.0
;   SEQ ID NO 6
;   LENGTH: 678
;   TYPE: DNA
;   ORGANISM: Discosoma sp
US-09-459-956-6

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Query Match        24.1%;  Score 256.6;  DB 3;  Length 678;
Best Local Similarity 62.8%;  Pred. No. 7.4e-74;
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Matches 419; Conservative   0; Mismatches 239; Indels   9; Gaps   1;

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Qy   102 AAGGGTGTGATTAAACCAGACATGAAGATGAAGCTGCGTATGGAAGGTGCTGTAAACGGG 161
         |||  |||||    |||||| |||||   ||  ||||||  || ||||||||| ||||||
Db    13 AAGAATGTTATCAAGGAGTTCATGAGAGTTTAAGGTTCGCATGGAAGGAACGGTCAATGGG 72

Qy   162 CACAAGTTCGTGGTTGAAGGAGATGGAAAAGGAGAAGCCTTTCGACGGAACACAGACTATG 221
         ||| ||||| ||  ||  || |||||| || |||   || |||| ||   |   |||   |
Db    73 CACGAGTTTGAAATAGAGAGGCGAGGAGGGGAGGGCCACATACCGAAGGCCACAATACCGTA 132

Qy   222 GACCTTACAGTCATAGAAGGCGCACCATTGCCTTTCGCTTACGATATCTTGCACAACAGTA 281
         ||| ||| |   ||   |  |  ||||  |||||||||||  |||| |||||| ||||||
Db   133 AAGCTTAAGGTAACCAAGGGACCTTTGCCATTTGCTTGGGATATTTTGTCACCACAA 192

Qy   282 TTCGATTACGGCAACAGCAGGGTATTCGGAACGAAGGTCATGAAGAGACATAGCAGATTATTTCAAG 341
         ||  ||  |||||||  ||| ||||  ||||||||||| |||||||||  |||||||||| |||
Db   193 TTTCAGTATGGAAGCAAGGTATATGTCAAGCACCCTGCCGACATACCAGACTATAAAAAG 252

Qy   342 CAGACGTTTCCTGAGGGGTACTTCTGGGAACGAACGATGACACATGACATCGATGAAGACACCAGGGCATT 401
         || ||||| |||| || ||| ||||||||||||||||| |||| |||| ||||||||||| |||
Db   253 CTGTCATTTCCTGAAGGATTTAAATGGGAAAGGGTCATGAACTTTGAAGACGGTGGCGTC 312

Qy   402 TGCATCGCCACAAACGACATAACAATGATGAAGGCGTCGACGACTGTTTTGCCTATAAA 461
         |||  || ||| ||  |||||||||  ||| || |  |
Db   313 GTTACTGTAACCCAGGATTCCAGTTGCAGGATGG--------CTGTTTCATCTACAAG 363

Qy   462 ATTCGATTTGATGGTGTGAACTTCCTGCCAATGGTCCAGTTATGCAGAGGAAGACGCTG 521
         || ||||  ||  |  || ||||  ||    | ||| |
Db   364 GTTACTTCATTGGCGTGAACTTTCCTTCCGATGGACCTGTTATGCAAAGAGAACAATG 423

Qy   522 AAATGGGAGGCCATCCACTGAGATAATGTATGCGCGTGATGGAGTGCTGAAGGGTGATGTT 581
         |||||||| ||||
Db   424 GGCTGGGAAGCCAGCAGCTGAGCGTTTGTATCCTCGTGATGGCGTGTTGAAAGGAGAGATT 483

Qy   582 AACATGGCTCTGTTGCTTGAAGGAGGTGGCCATTACCGATGTGACTTCAAAACTACTTAC 641
         |||| ||||| ||| || |||| ||
Db   484 CATAAGGCTCTGAAGCTGAAGACGGTGGTCATTACCTAGTTGAATTCAAAAGTATTTAC 543

Qy   642 AAAGCTAAGAAGGTTGTCCGGTTGCCAGACTATCACTTTGTTGTGGACCATCGCATTGAGATT 701
         || |||| |   ||||  ||  |  |  ||  ||  |||||  || |
Db   544 ATGGCAAAGAGCCTGTGCAGCTACCAGGGTACTACTATGTTGACTCCAAACTGGATATA 603

Qy   702 GTGAGCCACGACAAAGATTACACACAAGGTTAAGCTGCACGAGCATGCGAAGCTCGTCAT 761
         ||||| || |   |||||  | |   ||
Db   604 ACAAGGCCACACAACAGACTATACAATCGTTGACGCAGTATGAAAGAACCGAGGGACGCCCAC 663

Qy   762 GGACTGT 768
         |||||||
Db   664 CATCTGT 670
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RESULT 4
US-09-866-538-11
; Sequence 11, Application US/09866538
; Patent No. 6852849
; GENERAL INFORMATION:
;   APPLICANT: REGENTS OF THE UNIVERSITY OF CALIFORNIA
;   APPLICANT: TSIEN, Roger
;   APPLICANT: Campbell, Robert
;   TITLE OF INVENTION: NON-OLIGOMERIZING FLUORESCENT PROTEINS
;   FILE REFERENCE: REGEN1530-2
;   CURRENT APPLICATION NUMBER: US/09/866,538
;   CURRENT FILING DATE: 2001-05-24
;   NUMBER OF SEQ ID NOS: 29
;   SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
;   LENGTH: 859
;   TYPE: DNA
;   ORGANISM: Discosoma sp.
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (54)..(731)
US-09-866-538-11

Query Match   24.1%; Score 256.6; DB 3; Length 859;
Best Local Similarity 62.8%; Pred. No. 8.6e-74;
Matches 419; Conservative   0; Mismatches 239; Indels   9; Gaps   1;

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Qy   102 AAGGGTGTGATTAAACCAGACATGAAGATGAAGCTGCGTATGGAAGGTGCTGTAAACGGG 161
         |||  |||||    |||||| |||||   ||  ||||||  || ||||||||| ||||||
Db    66 AAGAATGTTATCAAGGAGTTCATGAGAGTTTAAGGTTCGCATGGAAGGAACGGTCAATGGG 125

Qy   162 CACAAGTTCGTGGTTGAAGGAGATGGAAAAGGAGAAGCCTTTCGACGGAACACAGACTATG 221
         ||| ||||| ||  ||  || |||||| || |||   || |||| ||   |   |||   |
Db   126 CACGAGTTTGAAATAGAGAGGCGAGGAGGGGAGGGCCACATACCGAAGGCCACAATACCGTA 185

Qy   222 GACCTTACAGTCATAGAAGGCGCACCATTGCCTTTCGCTTACGATATCTTGCACAACAGTA 281
         ||| ||| |   ||   |  |  ||||  |||||||||||  |||| |||||| ||||||
Db   186 AAGCTTAAGGTAACCAAGGGACCTTTGCCATTTGCTTGGGATATTTTGTCACCACAA 245

Qy   282 TTCGATTACGGCAACAGCAGGGTATTCGGAACGAAGGTCATGAAGAGACATAGCAGATTATTTCAAG 341
         ||  ||  |||||||  ||| ||||  ||||||||||| |||||||||  |||||||||| |||
Db   246 TTTCAGTATGGAAGCAAGGTATATGTCAAGCACCCTGCCGACATACCAGACTATAAAAAG 305

Qy   342 CAGACGTTTCCTGAGGGGTACTTCTGGGAACGAACGATGACACATGACATCGATGAAGACACCAGGGCATT 401
         || ||||| |||| || ||| ||||||||||||||||| |||| |||| ||||||||||| |||
Db   306 CTGTCATTTCCTGAAGGATTTAAATGGGAAAGGGTCATGAACTTTGAAGACGGTGGCGTC 365

Qy   402 TGCATCGCCACAAACGACATAACAATGATGAAGGCGTCGACGACTGTTTTGCCTATAAA 461
         |||  || ||| ||  |||||||||  ||| || |  |
Db   366 GTTACTGTAACCCAGGATTCCAGTTGCAGGATGG--------CTGTTTCATCTACAAG 416

Qy   462 ATTCGATTTGATGGTGTGAACTTCCTGCCAATGGTCCAGTTATGCAGAGGAAGACGCTG 521
         || ||||  ||  |  || ||||  ||    | ||| |
Db   417 GTCAAGTTCATTGGCGTGAACTTTCCTTCCGATGGACCTGTTATGCAAAGAGAACAATG 476

Qy   522 AAATGGGAGGCCATCCACTGAGATAATGTATGCGCGTGATGGAGTGCTGAAGGGTGATGTT 581
         |||||||| ||||
Db   477 GGCTGGGAAGCCAGCAGCTGAGCGTTTGTATCCTCGTGATGGCGTGTTGAAAGGAGAGATT 536

Qy   582 AACATGGCTCTGTTGCTTGAAGGAGGTGGCCATTACCGATGTGACTTCAAAACTACTTAC 641
         |||| ||||| ||| || |||| ||
Db   537 CATAAGGCTCTGAAGCTGAAGACGGTGGTCATTACCTAGTTGAATTCAAAAGTATTTAC 596

Qy   642 AAAGCTAAGAAGGTTGTCCGGTTGCCAGACTATCACTTTGTTGTGGACCATCGCATTGAGATT 701
         || |||| |   ||||  ||  |  |  ||  ||  |||||  || |
Db   597 ATGGCAAAGAGCCTGTGCAGCTACCAGGGTACTACTATGTTGACTCCAAACTGGATATA 656

Qy   702 GTGAGCCACGACAAAGATTACACACAAGGTTAAGCTGCACGAGCATGCGAAGCTCGTCAT 761
         ||||| || |   |||||  | |   ||
Db   657 ACAAGGCCACACAACAGACTATACAATCGTTGACGCAGTATGAAAGAACCGAGGGACGCCCAC 716

Qy   762 GGACTGT 768
         |||||||
Db   717 CATCTGT 723
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RESULT 5
US-09-865-291-11
; Sequence 11, Application US/09865291
; Patent No. 6900304
; GENERAL INFORMATION:
;   APPLICANT: REGENTS OF THE UNIVERSITY OF CALIFORNIA
;   APPLICANT: TSIEN, Roger
;   APPLICANT: TING, Alice
;   APPLICANT: ZHANG, Jin
;   TITLE OF INVENTION: EMISSION RATIOMETRIC INDICATORS OF PHOSPHORYLATION
;   FILE REFERENCE: REGEN1550
;   CURRENT APPLICATION NUMBER: US/09/865,291
;   CURRENT FILING DATE: 2001-05-24
;   NUMBER OF SEQ ID NOS: 42
;   SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
;   LENGTH: 859
;   TYPE: DNA
;   ORGANISM: Discosoma sp.

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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (54)..(731)
US-09-865-291-11

Query Match        24.1%;  Score 256.6; DB 3;  Length 859;
Best Local Similarity  62.8%;  Pred. No. 8.6e-74;
Matches 419;  Conservative   0;  Mismatches 239;  Indels   9;  Gaps   1;

Qy   102 AAGGGTGTGATTAAACCAGACATGAAGATGAAGAGTCGTGTATGGAAGGTGCTGTAAACGGG 161
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Db    66 AAGAATGTTATCAAGGAGTTCATGAGGTTTAAGGTTCGCATGGAAGGGAACCGGTCAATGGG 125

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Qy   282 TTCGATTACGGCAACAGGGTATTCGCCAAATACCAGAAGACATAGCAGATTATTTCAAG 341
             ||||| |||  ||||||  || |||| ||  |||||| ||| || | || |||||||||
Db   246 TTTCAGTATGGAAGCAAGGTATATGTCAAGCACATACCAGACTATAAAAAG 305

Qy   342 CAGACGTTTCCTGAGGGTACTTCTGGGAACGAAGCATGACATACGAAGACCAGGGCATT 401
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Db   306 CTGTCATTTCCTGAAGGATTAAATGGAAGGGTCATGAACTTTGAAGACGGTGCGTC 365

Qy   402 TGCATCGCCACAAAACGACATTAACAATGATGAGGCGTCGACAGTTTGCCTATAAA 461
             |||||||| ||  || ||| ||||| ||||| |||| |  |||||||||||||||
Db   366 GTTACTGTAACCCAGGATTCCAGTTTGCAGGATGG-------CTGTTTCATCTACAAG 416

Qy   462 ATTCGATTTGATGGTGTGAACTTCCTGCCAAATGGTCAGTTATGCAGAAGACGCTG 521
             |||||| || ||| || |||||||||||| ||||||||||| |||| ||||||||
Db   417 GTCAAGTTCATTGGGCGTGAACTTTCCTTCCGATGGACCTGTTATGCAAATGAGAACAATG 476

Qy   522 AAATGGGAGCCATCCACTGAGATAATGTATGCGCTGATGGAGTCGTGTTGTATCCGTGAAGGGTGATGTT 581
             |||||||||||| |||| ||||||||||||||||| ||  |||| |  | |||||| ||||| |||||
Db   477 GGCTGGGAAGCCAGCAGCCTGTGCAGCTACCAGGGTACTACATATGGGACGGTTGTTCCGTGTGTTGAAAGGAGAGATT 536

Qy   582 AACATGGCTCTGTTGCTTGAACGAGGAGGTGGCCATCCGATGATAATGTATCGCGTGACTTCAAAACTACTTAC 641
             |||||||||| | ||||| |||| ||| | |||| |||||||||||| ||||||| || | | ||||| ||||
Db   537 CATAAGGCTCTGAAGCTCTGAAAGACGGTGGTCATTACCTAGTTGAATTCAAAAGTATTTAC 596

Qy   642 AAAGCTAAGAAGGTTGTCCGGTTGCCAGACTATCACTTGTGGACCATCGCATTGAGATT 701
             |||||| |||||| ||||||  |||||| | ||||||| ||||||| ||| ||||| ||
Db   597 ATGGCAAGGAAGCCCTGTGCAGCTACCAGGGTACTACATATGTTGACTTCAAACTGGATATA 656

Qy   702 GTGAGCCACCACGACAAAGATTACAACAAGGTTAAGCTGCACGAGCCATGCCGAAGCTCGTCAT 761
             ||||||||||| ||||| || || |||||||||||||||||| ||||| ||||  || |||||
Db   657 ACAAGCCACAACGACGAAGACTATACAATCGTTGAGCAGTATGAAAGAACCGACGGAGGACGCCAC 716

Qy   762 GGACTGT 768
             |||||||
Db   717 CATCTGT 723
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RESULT 6
US-09-459-956-5
; Sequence 5, Application US/09459956
; Patent No. 6342379
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Gonzalez, III, Jesus E.
; TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY
; TITLE OF INVENTION: OPTICAL METHODS
; FILE REFERENCE: REGEN1290-4
; CURRENT APPLICATION NUMBER: US/09/459,956
; CURRENT FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 08/765,860
; PRIOR FILING DATE: 1999-05-08
; PRIOR APPLICATION NUMBER: 08/481,977
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; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: PCT/US96/09652
; PRIOR FILING DATE: 1996-06-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 699
; TYPE: DNA
; ORGANISM: Discosoma striata
US-09-459-956-5

Query Match        22.3%;  Score 237.2; DB 3;  Length 699;
Best Local Similarity  61.4%;  Pred. No. 1.9e-67;
Matches 421;  Conservative   0;  Mismatches 253;  Indels  12;  Gaps   2;

Qy   102 AAGGGTGTGATTAAACCAGACATGAAGATGAAGAGTCGTGTATGGAAGGTGCTGTAAACGGG 161
             |||| || |||    ||  |||||| |||| || || ||  | ||||||| || ||||||
Db    13 AAGAGTGTGATCAAGGAAGAAATGTTGATCGATCTTCATCTGGAGGAACGTTCAATGGG 72

Qy   162 CACAAGTTCGTGGTTGAAGGATGAAGAAAGGGAGGAGCCTTTCGACGGAACACAGACTATG 221
             |||||| || |||  || || || || ||  ||| || |||||||||| | |||||| ||
Db    73 CACTACTTTGAAATAAAAGGCAAAGGAAAAGGACAGCCACCAATACCGTC 132

Qy   222 GACCTTACAGTCATAGAAGGCCACCATTGCCTTTCGCGATTATCTTGACACAGTA 281
             |||||||||||| ||||  ||  ||||||| ||||| || || ||||| || ||
Db   133 ACGCTCGAGGTTACCAAGGGTGGACCTCTGCCATTTGGTTGGCATATTTGTGCCCACAA 192

Qy   282 TTCGATTACGGCAACAGGGTATTCGCCAAATACCAGAAGACATAGCAGATTATTTCAAG 341
             |||||||| || ||||  |||| |  ||  |||||||||| || || || || |||||
Db   193 TTTCAGTATGAAACAAGGCATTTGTCCACACCCTGACAACAATACATGATGATATCTAAAG 252

Qy   342 CAGACGTTTCCTGAGGGTACTTCTGGGAACGAAGCATGACATACGAAGACCAGGGCATT 401
             ||||||||| || || || |  |  |||||||| ||||| ||||||||| | ||||| |
Db   253 CTGTCATTTCCGGAGGGGATATACATGGAACATGGATCCATGCGAACTTTGAAGACGGTGGCTTG 312

Qy   402 TGCATCGCCACAAAACGACATTAACAATGATGAGGCGTCGACAGTTTGCCTATAAA 461
             |||||||| ||| || | |||| || | ||| |          |||||| ||||
Db   313 TGTTGTATCACCAATGATATCAGTTTGA------CAGGCAACTGTTTCTACTACGAC 363

Qy   462 ATTCGATTTGATGGTGTGAACTTCCTGCCAAATGGTCAGTTATGCAGAAGACGCTG 521
             ||||| || ||| || ||||||||||| | |||||||||| ||||| ||||||||
Db   364 ATCAAGTTCACTGGCTTGAACTTTCCTTCCAAATGGACCCGGTTGTGCAGAAGAGACAACT 423

Qy   522 AAATGGGAGCCATCCACTGAGATAATGTATCGCGTGACTTCAAAACTACTTAC 581
             |||||||||||| ||||||||| |||| | || |  | |||||||||| ||||
Db   424 GGCTGGGAACCGAGCACTGAGCGTTTGTATCCTCGTGATGTGCGATGTGTGTTGATAGGAGACATC 483

Qy   582 AACATGGCTCTGTTGCTTGAACGAGGAGGTGGCCATCCGATGATAATGTATCGCGTGACTTCAAAACTACTTAC 641
             ||||||| || | |||| || ||  |||| |||| |||||||| | || || ||||| | |||||| ||||||
Db   484 AACATGCTCTGACAGTTGAAGGAGGTGGTCATTACGCATGTGACATTAAAACTGTTTAC 543

Qy   642 AAAGCTAAGAAGGTTG---TCCGGTTGCCAGACTATCACTTGTGGACCATCCCATTCAG 698
             ||||| |||||||   ||||||| |||||| | ||||| || ||||| || ||||||
Db   544 AGGGCCAAGAAGGCCCGCCCTTGAAGATGCCAGGGTATCACATTGACAACCAAACTGTT 603

Qy   699 ATTGTGAGCCACCGACAAAGATTACAACAAGGTTAAGCTGCACGAGCCATGCCGAAGCTCGT 758
             |||| ||| ||| || ||  ||| |||| ||| |||| || |  ||||||  || |||||
Db   604 ATATGGAACACGACAAAGAATTCATGAAAGTTGAGGAGCATGAAATCGCCGTTGCACGC 663

Qy   759 CATGGACTGTCAAGGAAGGCCAAGTA 784
             ||| |  ||||||||||||
Db   664 CACCATCCGTTCTATGAGCCAAAGAA 689
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RESULT 7
US-10-152-296-1
; Sequence 1, Application US/10152296
; Patent No. 6723537
; GENERAL INFORMATION:
; APPLICANT: Peelle, Beau
; APPLICANT: Rigel Pharmaceuticals, Incorporated
; TITLE OF INVENTION: Directed Evolution of Protein in Mammalian Cells
; FILE REFERENCE: 021044-000110US
```

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;   CURRENT APPLICATION NUMBER: US/10/152,296
;   CURRENT FILING DATE: 2002-12-10
;   PRIOR APPLICATION NUMBER: US 60/291,871
;   PRIOR FILING DATE: 2001-05-18
;   NUMBER OF SEQ ID NOS: 2
;   SOFTWARE: PatentIn Ver. 2.1
;   SEQ ID NO 1
;   LENGTH: 723
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:mammalian
;   OTHER INFORMATION: codon-optimized variant (DsRED) of Discosoma sp.
;   OTHER INFORMATION: "red" red fluorescent protein (RFP)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(723)
;   OTHER INFORMATION: DsRED
US-10-152-296-1
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Query Match       20.9%;    Score 222.4;  DB 3;   Length 723;
Best Local Similarity  59.3%;  Pred. No. 1.5e-62;
Matches  401;  Conservative  0;  Mismatches 266;  Indels  9;  Gaps  1;

Qy   102 AAGGGTGTGATTAAACCAGACATGAAGATGAAGCTGCGTATGGAAGGTGCTGTAAACGGG 161
             ||  || | ||    |||| |     |||| | || || | || ||| | |
Db    16 AAGAACGTCATCAAGGAGTTCATCGCCTTCAAGTGCGATGGAGGGCACCGTGAACGGC  75

Qy   162 CACAAGTTCGTGGTTGAACGGAGATGGAAAAGGAAGCCTTTCGACGGACACAGACTATG 221
             ||||||||| | ||     |||| |  || ||  | |  |||||||||||||||
Db    76 CACGAGTTCGAGATCGAGGGCGAGGGCGAGGGCCGCCCCTACGAGGGCCACAACACCGTG 135

Qy   222 GACCTTACAGTCATAGAAGGCGCACCATTGCCTTGCCTTTCGCTTACGATATCTTGACAACAGTA 281
             |  |||||||| |   | ||| ||  ||| |||  || | ||||  |  | ||| || |
Db   136 AAGCTGAAGGTGACCAAGGGCGGCCCCCTGCCCTTCGCCTGGGACATCCTGTCCCCCCAG 195

Qy   282 TTCGATTACGGCAACAGCAGGGTATTGCCAAATACCCAGAGACATAGCAGATTATTTCAAG 341
             |||  |||||| ||||| || |||  |  ||| || | |  |||  ||| |||||| |||
Db   196 TTCCAGTACGGCTCCAAGTGTACGTGAAGCACCCCGCCGACATCCCCGACTACAAGAAG 255

Qy   342 CAGACGTTTCCTGAGGGGTACTTCTGGGAAACGAAGATCACACATGACGAAGACCAGGGCATT 401
             ||||||||||||||  |||  | | |  ||| |||||||| || |  | || ||||||||| |
Db   256 CTGTCCTTCCCCGAGGGCTTCAAGTGGGAGCGCGTGATGAACTTCGAGGACGGCGGCGTG 315

Qy   402 TGCATCGCCACAAAACGACGATAACAATGATGGAAGGCGTCGACGACTGTTTTTTGCCTATAAA 461
             ||  | ||| |     |  ||   |  | | |||||||
Db   316 GTGACCGTGACCCAGGACTCCCTGCCCGAG-------GACGGCGTGCTTCATCTACAAG 366

Qy   462 ATTCGATTTGATGTGTGAACTTTCCTGCCAATGTCCAGTTATGCAGAGGAAGACGCTG 521
             |  |  |||| |||||  | |||  |  |  ||||| || |  |||| ||| ||  |
Db   367 GTGAAGTTCATCGGCGTGAACTTCCCCTCCGACGGCCCCGTAATGCAGGCCCGTAATGCAGGACCATG 426

Qy   522 AAATGGGAGGCCATCCACTGAGATAATGTATGCGCGTGAAGGGTGCTGAAGGGTGATGTT 581
             ||  |  || || ||  |   | | |  | | || | ||||| | ||| |
Db   427 GGCTGGGAGGCCTGCACCAGCGCCTGTACCCCCGCGAGGGCGTGAAGGGCGAGATC 486

Qy   582 AACATGGCTCGTTGCTTGAGGAGGGTGGCCATTACCGATGTGACTTCAAAAACTACTTAC 641
             ||  |||||  |  | || || || ||  ||||||  ||  ||||  ||||  | ||||
Db   487 CACAAGGCCCTGAAGCTGAAGGACGGCGGCGTCCACTACCTGGTGGAGTTCAAGTCTGTGTAC 546

Qy   642 AAAGCTAAGAAGGTTGTCCGGTTGCCAGACTATCACTTTGTGGACCATCGCATTGAGATT 701
            |     ||  | || ||  ||| ||   | || ||||  | || ||   || |  ||
Db   547 ATGGCCAAGAAGCCCGTGCAGCTGCCCGGCTACTACTACGTGGACGTCCAAGCTGGACATC 606

Qy   702 GTGAGCCACCGACAAAGATTACAACAAGATTAAGCTGACAAGGTTAAGCTGACATGCCGAGCATGCGTCAT 761
            | |||| || |  |  | | | |    ||  ||  | ||   | | ||| || || ||
Db   607 ACCTCCCACAACGAGGACTACACCATCGTGGAGCAGTACGAGCGCGCACCGAGGGCCGGCCAC 666

Qy   762 GGACTGTCAAGGAAGG 777
            ||||| |||||| |||
Db   667 CACCTGTTCCTGGAGG 682
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RESULT 8
US-10-001-189-45
;   Sequence 45, Application US/10001189
;   Patent No. 6962810
;   GENERAL INFORMATION:
;   APPLICANT: FRASER JR., MALCOLM J.
;   APPLICANT: LI, XU
;   APPLICANT: BEAM, TERESA
;   TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TRANSPOSITION USING
;   TITLE OF INVENTION: MINIMAL SEGMENTS OF THE EUKARYOTIC TRANSFORMATION
;   TITLE OF INVENTION: VECTOR PIGGYBAC
;   FILE REFERENCE: 835910-92098
;   CURRENT APPLICATION NUMBER: US/10/001,189
;   CURRENT FILING DATE: 2001-10-30
;   PRIOR APPLICATION NUMBER: 60/244,984
;   PRIOR FILING DATE: 2000-11-01
;   PRIOR APPLICATION NUMBER: 60/244,677
;   PRIOR FILING DATE: 2000-10-31
;   NUMBER OF SEQ ID NOS: 70
;   SOFTWARE: PatentIn Ver. 2.1
;   SEQ ID NO 45
;   LENGTH: 6984
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:
;   OTHER INFORMATION: pBXP3-DsRed-orf sequence
US-10-001-189-45
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Query Match        20.6%;    Score 219.8;  DB 3;   Length 6984;
Best Local Similarity  59.4%;  Pred. No. 4.0e-61;
Matches  396;  Conservative  0;  Mismatches 262;  Indels  9;  Gaps  1;

Qy   102 AAGGGTGTGATTAAACCAGACATGAAGATGAAGCTGCGTATGGAAGGTGCTGTAAACGGG 161
             ||  || | ||    |||| |     |||| | || || | || ||| | |
Db  2986 AAGAACGTCATCAAGGAGTTCATCGCCTTCAAGTGCGATGGAGGGCACCGTGAACGGC 3045

Qy   162 CACAAGTTCGTGGTTGAACGGAGATGGAAAAGGAAGCCTTTCGACGGACACAGACTATG 221
             ||||||||| | ||     |||| |  || ||  | |  |||||||||||||||
Db  3046 CACGAGTTCGAGATCGAGGGCGAGGGCGAGGGCCGCCCCTACGAGGGCCACAACACCGTG 3105

Qy   222 GACCTTACAGTCATAGAAGGCGCACCATTGCCTTGCCTTTCGCTTACGATATCTTGACAACAGTA 281
             |  |||||||| |   | ||| ||  ||| |||  || | ||||  |  | ||| || |
Db  3106 AAGCTGAAGGTGACCAAGGGCGGCCCCCTGCCCTTCGCCTGGGACATCCTGTCCCCCCAG 3165

Qy   282 TTCGATTACGGCAACAGCAGGGTATTGCCAAATACCCAGAGACATAGCAGATTATTTCAAG 341
             |||  |||||| ||||| || |||  |  ||| || | |  |||  ||| |||||| |||
Db  3166 TTCCAGTACGGCTCCAAGTGTACGTGAAGCACCCCGCCGACATCCCCGACTACAAGAAG 3225

Qy   342 CAGACGTTTCCTGAGGGGTACTTCTGGGAAACGAAGATCACACATGACGAAGACCAGGGCATT 401
             ||||||||||||||  |||  | | |  ||| |||||||| || |  | || ||||||||| |
Db  3226 CTGTCCTTCCCCGAGGGCTTCAAGTGGGAGCGCGTGATGAACTTCGAGGACGGCGGCGTG 3285

Qy   402 TGCATCGCCACAAAACGACGATAACAATGATGGAAGGCGTCGACGACTGTTTTTTGCCTATAAA 461
             ||  | ||| |     |  ||   |  | | |||||||
Db  3286 GTGACCGTGACCCAGGACTCCCTGCCCGAG-------GACGGCGTGCTTCATCTACAAG 3336

Qy   462 ATTCGATTTGATGTGTGAACTTTCCTGCCAATGTCCAGTTATGCAGAGGAAGACGCTG 521
             |  |  |||| |||||  | |||  |  |  ||||| || |  |||| ||| ||  |
Db  3337 GTGAAGTTCATCGGCGTGAACTTCCCCTCCGACGGCGTAATGCAGGAAGAAGACCATG 3396

Qy   522 AAATGGGAGGCCATCCACTGAGATAATGTATGCGCGTGAAGGGTGCTGAAGGGTGATGTT 581
             ||  |  || || ||  |   | | |  | | || | ||||| | ||| |
Db  3397 GGCTGGGAGGCCTGCACCAGCGCCTGTACCCCCGCGAGGGCGTGAAGGGCGAGATC 3456

Qy   582 AACATGGCTCGTTGCTTGAGGAGGGTGGCCATTACCGATGTGACTTCAAAAACTACTTAC 641
             ||  |||||  |  | || || || ||  ||||||  ||  ||||  ||||  | ||||
Db  3457 CACAAGGCCCTGAAGCTGAAGGACGGCGGCGTCCACTACCTGGTGGAGTTCAAGTCTGTGTAC 3516

Qy   642 AAAGCTAAGAAGGTTGTCCGGTTGCCAGACTATCACTTTGTGGACCATCGCATTGAGATT 701
            |     ||  | || ||  ||| ||   | || ||||  | || ||   || |  ||
Db  3517 ATGGCCAAGAAGCCCGTGCAGCTGCCCGGCTACTACTACGTGGACGTCCAAGCTGGACATC 3576
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Db   702 GTGAGCCACGACAAAGATTACACAAGGTTAGCTGCGAGCATGCCGAAGCTCGTCAT 761
             ||||||||||  ||  |||  ||  ||  ||||||  ||||||  |||||
Db  3577 ACCTCCCACAACGAGAGACTACACCATCGTGGAGCAGTACGAGCGCGCCGAGGAGGCCGCCCAC 3636

Qy   762 GGACTGT 768
             |||||
Db  3637 CACCTGT 3643
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RESULT 9
US-09-459-956-2
; Sequence 2, Application US/09459956
; Patent No. 6342379
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Gonzalez, III, Jesus E.
; TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY
; TITLE OF INVENTION: OPTICAL METHODS
; FILE REFERENCE: REGEN1290-4
; CURRENT APPLICATION NUMBER: US/09/459,956
; CURRENT FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 08/765,860
; PRIOR FILING DATE: 1999-05-08
; PRIOR APPLICATION NUMBER: 08/481,977
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: PCT/US96/09652
; PRIOR FILING DATE: 1996-06-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 690
; TYPE: DNA
; ORGANISM: Anemonia majano
US-09-459-956-2

Query Match   19.5%; Score 208; DB 3; Length 690;
Best Local Similarity 59.2%; Pred. No. 8.2e-58;
Matches 399; Conservative 0; Mismatches 260; Indels 15; Gaps 2;

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Qy    91 TTGCACAGGAAAAGGGTGTGATTAAACCAGACATGAAGATGAAGCTGCGTATGGAAGGTG 150
            ||  ||   |  |||  |||  |||| ||| ||||||||| ||||| |||||  |||| |
Db     2 TGGCTCTTTCAAACAGTTTATCGGAGGATGACATGAAGATGACCTACCATATGGATGGCT 61

Qy   151 CTGTAAACGGCACCAGCAAGTTCGTTGGTTGAAGGAGATGAAGATGAAGCCTTCGACGGCA 210
            ||||||| |||||  | |||   ||  |  |||||| |||  | |||||||| |||| ||
Db    62 GTGTCAATGGGCATTACTTTAAAGTCACCATGGCCAACAGGGTATTCCGCCCCCTGGGGGA 121

Qy   211 CACAGACTATGACCTTACAGTCA------TAGAAGGCGCACCATTGCCTTTCGCTTACG 264
            ||| | | ||| |||  ||| ||       || ||||| |||| |  | ||| ||||||
Db   122 CGCAGGACTTCGACTTTTAAAGTCACCATGGCCAACAGGGTATTCCGCCCCCTGGGGGA 181

Qy   265 ATATCTTGACAACAGTATTCGATTACGGCAACAGGTATTCGATGCTTTACTCGCGTATCCT 324
            |||| | ||||  | | |   | | ||| || ||| |||| | | |||||| |||| |||
Db   182 ACATACTACTCACAGTGTTCAAAATCTCTGGGAACAGGTGTCATCTTTCCGAAGACAGTA 241

Qy   325 TAGCAGATTATTTCAAGCAGCAGACGCGTTTCCTGAGGGGTACTTCTGGGAACAGCATGACAT 384
            |||| ||| ||  ||||| | | ||  ||  |||| |||  |||  ||||||| |||||||
Db   242 TGCCCGACTATTTCAAACAAGACATTTCCTGACGGGAGTGCATAGGACTTTTTTACCT 301

Qy   385 ACGAAGACCAGGCATTTGCATCGCCACAACAACGACATAACAAGATGAAGGCGTCGACG 444
            | |||| | |||| ||||  ||| ||||||| ||| |||||||| ||| ||||| ||
Db   302 ATGAAGATGAGGAGTTGCTACAGCCAGTTGCTACAGCCAGTTGGGAAATAAGCCTTAA------AGGCA 352

Qy   445 ACTGTTTTGCCTATAAAATTCGATTTGATGGGTGACCTTCCTGCCAATGTCCAGTTA 504
            || || || | |||  | | |||  |||| | |||||| |||| | |||||| |||
Db   353 ACTGCTTTGAGCACAAATCCCACGTTTCATGGAGTGAACTTTCCTGCTGCTGATGACCTGTGA 412

Qy   505 TGCAGGAAGAGCGCTGAAATGGGAGCCATCCACTGGAGATAATGTATGCGCGTGATGGAG 564
             |||||| || | |||| |||||  ||| ||||  |||  |||| |||  | ||||||||
Db   413 TGGCGGAAGAACAACTGGTTGGGTGGACCCATCCATTCTTGAGAAAATGACTGTGCGGATGGAA 472

Qy   565 TGCTGAAGGGTGATGTTAACATGGCTCTGTTGCTTGCAGGAGGTGGCCATTACCGATGTG 624
            ||||||| |||  | ||  |||||  | |  ||  | || ||  || || ||||  |||
Db   565 ...
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Db   473 TATTGAAGGGTGATGTCACCGCGTTCCTCATGCTGCGCAAGGAGGTGGCAATTACAGATGCC 532
Qy   625 ACTTCAAACTACTTACAAGCTAAGAAGCTTGTCCCGTTGTGTCCAGATCTATCACTTCGTGG 684
Db   533 AATTCCACACTTCTTACAAGACAAAAAACCGGTGACGATGCCACCAAACCATGTGGTGG 592
Qy   685 ACCATGCCATTGAGATTGTGAGCACCAGACAAAGATTACAACAAGGTTAAGCTGCACGAGC 744
Db   593 AACATGCCATTGCGACGACCACCTTGACAAAGGTGCAACAGTGTTGACTGACGGAGC 652
Qy   745 ATGCCGAAGCTCGT 758
Db   653 ACGCTGTTGCACAT 666
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RESULT 10
US-09-459-956-4
; Sequence 4, Application US/09459956
; Patent No. 6342379
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Gonzalez, III, Jesus E.
; TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY
; TITLE OF INVENTION: OPTICAL METHODS
; FILE REFERENCE: REGEN1290-4
; CURRENT APPLICATION NUMBER: US/09/459,956
; CURRENT FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 08/765,860
; PRIOR FILING DATE: 1999-05-08
; PRIOR APPLICATION NUMBER: 08/481,977
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: PCT/US96/09652
; PRIOR FILING DATE: 1996-06-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 696
; TYPE: DNA
; ORGANISM: Zoanthus sp
US-09-459-956-4

Query Match   16.7%; Score 177.8; DB 3; Length 696;
Best Local Similarity 59.5%; Pred. No. 7.6e-48;
Matches 340; Conservative 0; Mismatches 222; Indels 9; Gaps 2;

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Qy    91 TTGCACAGGAAAAGGGTGTGATTAAACCAGACATGAAGATGAAGCTGCGTATGGAAGGTG 150
Db     2 TGGCTCATTCAAAGCACGACGCGTCTAAAGAAGAAGAAAATGACATGAAATACCACATGGAAGGGT 61
Qy   151 CTGTAAACGGCACCAGCAAGTTCGTTGGTTGAAGGAGATGAAGATGAAGCCTTCGACGGAA 210
Db    62 GCGTCAACGGACATAAATTTGTGATCACGGGCGAAGGCATTGGATATCCGTTCAAAGGGA 121
Qy   211 CACAGACTATGACCTTACAGTCATCATAGAAGGCGCACCATTGCCTTTCGCTTACGATATCT 270
Db   122 AACAGACTATTAATCTGTGTGTGTGATCGCAACAGGGGGACCATTGCCATTTTCCGAAGACAGATAT 181
Qy   271 TGACAACAGTATTCGATTACGGCAACAGGGTATTCGGCAACATACCCAGAAGACATAGCAG 330
Db   182 TGTCAGCTGGCGCTTTAAGTACGGACACGGAGATTGGGCAGAGGGGACCATTTTCCTGAAGACACATAGTAG 241
Qy   331 ATTATTTCAAGCAGCAGACGCGTTTCCTGAGGGGTACTTCTGGGACAATGGGACAGAAG 390
Db   242 ACTATTTCAAGAACTGCGTGTCCTGGGATATAACATGGGGCAGGTCTTTTTCTCTTTGGG 301
Qy   391 ACCAGGCAGTTTGCATCGCCACAACGAACATAACAACATGAGGAAGGCGTCGACGCTGTT 450
Db   302 ATGGAGCAGTCTGCCATATGCAATGATAACAACATGAGATAATAACAGTGA---GTGTCAAAGAAAACTGCA 358
Qy   451 TTGCCTATAAAATTCGATTGATGGTGTGAACTTTCCTGCCAATGGTCCAGTTATGCGAGA 510
Db   359 TTTATCATAAGAGCATATTTAATGAAGTGAATATTTCTCTGCTGCTGATGAATGAAAAA 418
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Qy   511 GGAAGAGCTGAAATGGGAGCCATCCACTGAGATAATGTATGCGCGTGAT------GGAG 564
           ||||| ||| ||||| ||| ||||
Db   419 AGATGACAGATAACTGGGAGCATCCTGCCGAGAAGATCATACCAGTACCTAAGCAGGGGA 478

Qy   565 TGCTGAAGGGTGATGTTAACATGGCTCTGTTGCTTGAAGGAGGTGGCCATTACCGATGTG 624
           || || ||||| || ||||
Db   479 TACTGAAAGGGGATGTGTCTCCATGTACCTCCTTCTGAAGGATGGTGGCGTTTACGGTGCC 538

Qy   625 ACTTCAAAACTACTTACAAAGCTAAGAAGT 655
           | |||| ||||||||| ||||
Db   539 AGTTCGACACAGTTTACAAAGCAAAGTCTGT 569

RESULT 11
US-09-459-956-3
; Sequence 3, Application US/09459956
; Patent No. 6342379
; GENERAL INFORMATION:
;   APPLICANT: Tsien, Roger Y.
;   APPLICANT: Gonzalez, III, Jesus E.
;   TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY
;   TITLE OF INVENTION: OPTICAL METHODS
;   FILE REFERENCE: REGEN1290-4
;   CURRENT APPLICATION NUMBER: US/09/459,956
;   CURRENT FILING DATE: 1999-12-13
;   PRIOR APPLICATION NUMBER: 08/765,860
;   PRIOR FILING DATE: 1999-05-08
;   PRIOR APPLICATION NUMBER: 08/481,977
;   PRIOR FILING DATE: 1995-06-07
;   PRIOR APPLICATION NUMBER: PCT/US96/09652
;   PRIOR FILING DATE: 1996-06-06
;   NUMBER OF SEQ ID NOS: 22
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 696
;   TYPE: DNA
;   ORGANISM: Zoanthus sp
US-09-459-956-3

Query Match   16.5%;   Score 176.2;   DB 3;   Length 696;
Best Local Similarity 59.4%;   Pred. No. 2.6e-47;
Matches 339;   Conservative   0;   Mismatches 223;   Indels   9;   Gaps   2;

Qy   91 TTGCACAGGAAGAAAGGGTGTGATTAAACCAGACATGAAGAGTGAAGCTGCCTATGGAAGTG 150
           ||||| || ||| ||| ||||||| |||| ||||
Db   2 TGGTTCAGTCAAAGCACCGTCTAACAAAAGAAATGAACATGAAATACCGTATGAAAGGGT   61

Qy   151 CTGTAAACGGGCACAAGTTCGTTGGTTGAAGGATGTGAAGAAAGGGAAGCCTTTCGACGGAA 210
           |||||| |||||||||||| |||| || | || ||||
Db   62 GCGGTCGATGGACATAAAATTTGTGATCACGGGAGAGGCGATTGTGATATCCGTTCAAAGGGA 121

Qy   211 CACAGACATGGGACCTTACAGTCATCAGAGAGGCCGCACCATTGCCCTTCGCTTACGATATCT 270
           ||||||||||| || ||||||||| |||| | ||||
Db   122 AACAGGGCTATTAATCTGTCTGTGTGGTCGGAAGGTGGACCGTGAAGGTGCCGAAGAACATAT 181

Qy   271 TGACAACAGTATTCGATTACGGCGCAACAGGGTATTCGCCAAATACCCAGAAGAACATACAG 330
           ||||||||| |||| ||||| | |||| ||||||||| |||||
Db   182 TGTCAGCTGCCTTTAACTACGGAAAACAGGGTTTTCACTGAATATCCTCAAGACAATAGTTG 241

Qy   331 ATTATTTCAAGCAGACGTTTCTGAGGGGTACTTCTGGGAACGCATGACATACGAAG 390
           ||||| | ||||||||||| |||||||||||| ||||||
Db   242 ACTATTTCAGAGAACTCGTGTCGTCTGCTGATAATGGGACAGGTGTTTTCTCTTGAGG 301

Qy   391 ACCAGGGCATTTGCATCGCCACAACAGACGACTACAACAATGATGGAAGGCGTCGACGACTGTT 450
           ||||||| |||||||||||
Db   302 ATGGAGCAGTTGCATATGAGTCAGATATAACAGTGA---GTGTTGAAGAAAACTGCA 358

Qy   451 TTGCCTATAAAATTCGATTTGATTGTGTGAACTTCCTGCCAATGGTCCAGTTATGCGAGA 510
           |||| |||||| | |||| ||||| || ||||||| |
Db   359 TGTATCATGAGTCCAAATTTTATGGAGTGAATTTCCTGCTGATGGACCTGTGTGATGAAAA 418

Qy   511 GGAAGACGCTGAAATGGGAGCCATCCACTGAGATAATGTATGCGCGTGAT------GGAG 564
           |||| | ||||| |||

Db 539 ACTACAGCTGCCACATGAAGACCTTCACCGGAGCAAGGGCGGCGTGAAGGAGTTCCCTG 598

Qy 673 ATCACTTTGTGGACCATCGCATTGAGATTGTGAGCCACGACAAAGATTACAACAAGGTTA 732

Db 599 AGTACCTATTCATCCACCACCGCGGTGGAGAAGAACTACGTGGAGGAGGGCAGCTTCGTGG 658

Qy 733 AGCTGCACGAGCGATGCCGAAGCTC 756

Db 659 AGCAGCACGACCGAGCCGCCATCGCCC 682

RESULT 13
US-10-021-818A-1
; Sequence 1, Application US/10021818A
; Patent No. 6936428
; GENERAL INFORMATION:
; APPLICANT: Davis, Ronald W.
; TITLE OF INVENTION: Dimeric Fluorescent Polypeptides
; FILE REFERENCE: 25436/1652
; CURRENT APPLICATION NUMBER: US/10/021,818A
; CURRENT FILING DATE: 2001-12-13
; PRIOR APPLICATION NUMBER: US 60/256,121
; PRIOR FILING DATE: 2000-12-15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Renilla reniformis
US-10-021-818A-1

Query Match   12.4%;   Score 132.2; DB 3;   Length 720;
Best Local Similarity 54.4%;   Pred. No. 8.7e-33;
Matches 316; Conservative   0; Mismatches 253;   Indels 12; Gaps   2;

Qy 122 CATGAAGATGAAGCTGGGTATGGGAAGTGCTGTAAACGGGCACAAGTTCGTGGTTGAAGG 181

Db   45 CATGTCGTTTAAAGTGAATCTGGAAGGTGTAGTAAACAATCATGTGTTCACCAAGTGGAAGG 104

Qy 182 AGATGGAAAAGGGAAGCCTTTCGACCGAACACAGACTATGGACCTTACAGTCATGAAGG 241

Db 105 TTGTGGAAAAGGAAATATTTTATTCGGAAACCAACTTGGTTCAGATTCGTGTCACAAAAGG 164

Qy 242 CGCACCATTGCCTTTCGCTTACGATATCTTGACAACAGTATTCGATTACGGCAACAGGGGT 301

Db 165 GGTCCCGCTTCCATTTGCATTTGATATTTCTCTCCACCAGCTTTCCAATACGGCAACCGTAC 224

Qy 302 ATTCGCCAAATACCCAGAAGACATAGCACAGATTATTTCAAGCAGACGTTTCCTGAGGGGTA 361

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Qy 362 CTTCTGGGAACGAAGCAGAAGACGACCAGGGCATTTGCATCGCCACAAACGACAT 421

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Qy 422 AACAATGCATGAGAGGCCTCGACGACTGTTTGCCTATAAAATTCGATTGATGGTGTGAA 481

Db 345 AAATTTAA--------TCGAGGAGATGTTTGTCTTACGAGTGGAATATAAAGGTAGTAA 395

Qy 482 CTTTCCTGCCAATGGTCAGTTATGCAGAGAAGACGCTGAAATGGGAGCCATCCACTGA 541

Db 396 CTTCCCGACGATGGTCCAGTGATGAGAAGTGAGAAGATTACACAGGATTACAACCTTCGTTCGA 455

Qy 542 GATAATGTATGCGCGTGATGAGTCGGTGATGTTAACATGGCTCTGTTGCTTGA 601

Db 456 AGTTGTGTATATGAACGATGGGCGTCTTGGTTGGCCAAGTCATTCTTGTTTATAGATTAAA 515

Qy 602 AGGAGGTGGCCATTACCGATGTGACTTCAAAACTACTTACAAAGCTAAGAACGTTGTTCCG 661

Db 516 CTCTGGCAAATTTATTCGTGTCGTCACATGAGAACACTGATGAAATCAAAGGGGTGTAGTGAA 575

Qy 662 G---TTGCCAGACTATCACTTTGTGTGGACCATCGCATTGAGA 699

Db 576 GGATTTTCCCGAATACCATTTCATTCAACATCGTTTAGAGA 616

RESULT 14
US-09-839-650-1
; Sequence 1, Application US/09839650
; Patent No. 6645761
; GENERAL INFORMATION:
; APPLICANT: Stratagene
; TITLE OF INVENTION: Humanized Polynucleotide Sequence Encoding Renilla Mulleri Green
; Patent No. 6645761
; TITLE OF INVENTION: Fluorescent Protein
; FILE REFERENCE: 25436/1755
; CURRENT APPLICATION NUMBER: US/09/839,650
; CURRENT FILING DATE: 2001-04-19
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized R. mulleri polynucleotide
; NAME/KEY: misc_feature
; LOCATION: (1)..(720)
; OTHER INFORMATION: Humanized DNA sequence
US-09-839-650-1

Query Match   11.8%;   Score 126; DB 3;   Length 720;
Best Local Similarity 51.3%;   Pred. No. 9.7e-31;
Matches 325; Conservative   0; Mismatches 300;   Indels   9; Gaps   1;

Qy 123 ATGAAGATGAAGCTGCGTATGGGAAGGTGCTGTAAACGGGCACAAGTTCGTGGTTGAAGGA 182

Db   46 ATGAGCTACAAGGTGAACCTGGAGGGCATCGTGAACAACACCACGTGTTCACCATGGAGGGC 105

Qy 183 GATGGAAAAGGGAAGCCTTTCGACCGAACAGACTATGGACCTTACAGTCATAGAAGGC 242

Db 106 TGCGGCAAGGGCAACATCCTGTTCGGCAACATCTTGACAACAGTATTCGATTACGGCAACAGGGTA 165

Qy 243 GCACCATTGCCTTTCGCTTACGATATCTTGACAACAGTATTCGATTACGGCAACAGGGTA 302

Db 166 GCCCCCCCTGCCCTTCGCCCTTCGACATCGTGACCGCCCTTCCAGTACGGCAACCGCACC 225

Qy 303 TTCGCCAAATACCCAGAAGACATAGCACAGATTATTTCAAGCAGACGTTTCCTGAGGGGTAC 362

Db 226 TTCACCAAGTACCCCCAGACGACATCAGCCAGCACCTTCATCCGAGCTTCCAGCGGGTTC 285

Qy 363 TTCTGGGAACGAAGCAGAAGACATGACAGCCAGGGCATTTGCATCGCCACAAACGACATA 422

Db 286 ATGTACGAGCGACCACCCGCGCTACGAGGAGGACGGCGCCTGGTGGAGATCCGCAGCGCACATC 345

Qy 423 ACAATGATGGAAGGCCTCGACGACTGTTTGCCTATAAAATTCGATTGATGGTGTGAAC 482

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Qy 483 TTTCCTGCCAATGGTCAGTTATGCAGAGAAGACGCTGAAATGGGAGCCATCCACTGAG 542

Db 397 TTCCCCGACGACGGCCCCGTGATGCAGAAGAAGACCATCGGGCTGGGAGGCTCTCGTTGCTTGAA 456

Qy 543 ATAATGTATGCGCGTGATGAGTCGGTGATGTTAACATGGCTCTGTTGCTTGAAC 602

Db 457 GCCATGTACATGAACAACGGGGCGTGCTGTGGCGAGGTGATCGTTGGTGTACAAGCTGAAC 516

Qy 603 GGAGGTGGCCATTACCGATGTGACTTCAAAACTACTTACAAAGCTAAGAAGGTTGTCCGG 662

Db 517 AGCGGCAAGTACTACAGCTGCCACATGAAGCTGCCATTGTGGACCATTGAGATTGTGAAG 576

Qy 663 TTGCCAGACTATCACTTTGTGTGGACCATCGCATTCATCCAGCCACCACGCCGCCTACGTGGAGGACGGC 722

Db 577 GAGTTCCCCTCCTACACTTCATCCAGCCACCACGCCGCCTACGTGGAGGACGGC 636

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Qy   517  AGCGGCAAGTACTACAGCTGCCACATGAAGACCCTGATGAAGAGCAAGGGCGTGGTGAAG 576
          ||| |||||||  |  ||  |||  || |||  |||||||  |||| |||||| ||| |||
Db   517  ...

Qy   663  TTGCCAGACTATCACTTTGTGGACCATCGCATTGAGATTGTGAGCAAACGACAAAGATTAC 722
          |||||| || || |||||  |  |||||| ||||| ||| || ||||| ||  ||  ||||
Db   577  GAGTTCCCCTCCTACCACTTCATCCAGCACCAGCGCCTGGAGAAGACCTACGTGGAGGACGGC 636

Qy   723  AACAAGGTTAAGCTGCACGAGCATGCCGAAGCTC 756
          ||| |||||  ||  |||||||||  || |||||
Db   637  GGCTTCGTGGAGCAGCAGCAGGACCGCCATCGCCC 670
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RESULT 15
US-10-652-703A-1
; Sequence 1, Application US/10652703A
; Patent No. 6884620
; GENERAL INFORMATION:
; APPLICANT: Stratagene
; TITLE OF INVENTION: Humanized Polynucleotide Sequence Encoding Renilla Mulleri Green
; Patent No. 6884620
; TITLE OF INVENTION: Fluorescent Protein
; FILE REFERENCE: 25436/1754
; CURRENT APPLICATION NUMBER: US/10/652,703A
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US09/839,650
; PRIOR FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US09/748,786
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Humanized R. mulleri polynucleotide
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(720)
; OTHER INFORMATION: Humanized DNA sequence
US-10-652-703A-1

Query Match   11.8%;   Score 126; DB 3;   Length 720;
Best Local Similarity 51.3%;   Pred. No. 9.7e-31;
Matches 325; Conservative   0; Mismatches 300; Indels   9; Gaps   1;

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Qy   123  ATGAAGATGAAGCTGCGTATGGAAGGTGCGTAAACGGGCACAAGTTCGTGGTTGAAGGA 182
          |||  | |   |||  || ||| ||  ||   |||  | ||  |||  | |||| |||||
Db    46  ATGAGCTACAAGGTGAACCTGGAGGGCATCGTGAACAACCACGTGTTCACCATGGAGGGC 105

Qy   183  GATGGAAAAGGGAAGGCCTTTCGACGAACACAGACTATGGACCTTACAGTCATAGAAGGC 242
          ||| || |  ||  ||  ||| | ||  |  || || || |||   ||| ||||| ||||
Db   106  TGCGGCAAGGGCAACATCCTGTTCGGCAACCAGCTGCGCCACCAGCTGGAGATCCGCGTGACCGAGGGC 165

Qy   243  GCACCATTGCCTTTCGCTTACGATATCTTGACAACAGTATTCGATTACGGCAACACAGGGTA 302
          || |   | ||  ||||  |  |  ||  ||  || ||  | ||   |||  || || || |
Db   166  GCCCCCTGCCCTTCGCCTTCGACATCGTGGCCCGCCTTCCAGTACGGCAACCACCGCACC 225

Qy   303  TTCGCCAAATACCCAGAAGACATAGCAGATTATTTCAAGCAGACGTTTCCTGAGGGGTAC 362
          | |  |||| || ||||| || |  || || || || ||| ||  || || ||| ||
Db   226  TTCACCAAGTACCCCAACGACATCAGCGACTACTTCATCCAGCAGCTTCCCCGCGGCTTC 285

Qy   363  TTCTGGGAACGAAGCATGACAATACGAAGACATCAGCGCATTGCATCGCCACAAACGACATA 422
          || |  |||  |  || || || |  ||  || |   | ||  || |||  || |  || |
Db   286  ATGTACGAGCGACCCGCACCCTGCGCTAGCAGGAGCGGCGCCCTGGTGGAGATCCGCAGCGACATC 345

Qy   423  ACAATGATGGAAGGCGTCGACGACGTGTTTGCCTATAAAATTCGATTTGATGGTGTGAAC 482
          |  | | |  |||  |  || || |||  |  || ||  || ||| ||| |  || ||||
Db   346  AACCTGA-------TCGAGGACAAGTTCGTGTACCGCGTGAGTACAAGGGCAGCAAC 396

Qy   483  TTTCCTGCCAATGTCCAGTTATGCAGGAAGACGCTGAAATGGAGCCATCCACTGAG 542
          |||   || |  | || || || ||  || |   ||  || ||  ||| |  || ||
Db   397  TTCCCCGACGACGCCCCCGTGATGCAGAAGAAGACCATGGGCTGGGAGGCCTCCACCGAG 456

Qy   543  ATAATGTATGCGCGTGATGGAGTGCTGAAGGGTGCTTAACATGGCTCGTGTTGCTTGAA 602
          || | | | | |  ||||  ||  ||  |||  |||  || ||  ||  || || || |
Db   457  GCCATGTACATGAACAACGCCCGCTTCTTGGTGGGCGCAGGTGTATCCTGGTGTACAAGCTGAAC 516

Qy   603  GGAGGTGGCCATTACCGATGTGACTTCAAAACTACTTACAAACGGTTGTCCGG 662
          ||  || |   ||   ||  ||  ||   |  | |  || ||  |||  || |
Db   517  ...
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OM nucleic - nucleic search, using sw model

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            GenCore version 5.1.7
    Copyright (c) 1993 - 2006 Bioacceleration Ltd.
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Run on: April 5, 2006, 21:02:02 ; Search time 1060 Seconds
                                       (without alignments)
                                    8316.186 Million cell updates/sec

Title: US-10-757-356-17
Perfect score: 1066
Sequence: 1 attcgcccgtggtgattgga.........atcgaagccgaaaaaaaaa 1066

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published Applications_NA_Main:*
                1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
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                9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
               10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description | | |
|---|---|---|---|---|---|---|---|---|
| 1 | 1066 | 100.0 | 1066 | 8 | US-10-757-356-17 | Sequence 17, Appl | | |
| 2 | 838.8 | 78.7 | 913 | 8 | US-10-757-356-25 | Sequence 25, Appl | | |
| 3 | 665 | 62.4 | 1133 | 8 | US-10-757-356-27 | Sequence 27, Appl | | |
| 4 | 628 | 58.9 | 684 | 7 | US-10-314-827-21 | Sequence 21, Appl | | |
| 5 | 628 | 58.9 | 684 | 7 | US-10-314-827-1 | Sequence 1, Appl | | |
| 6 | 628 | 58.9 | 684 | 10 | US-11-021-014-7 | Sequence 7, Appli | | |
| 7 | 626.4 | 58.8 | 684 | 8 | US-10-314-936-5 | Sequence 5, Appli | | |
| 8 | 626.4 | 58.8 | 684 | 10 | US-11-021-014-5 | Sequence 5, Appli | | |
| 9 | 533.4 | 50.0 | 795 | 8 | US-10-757-356-15 | Sequence 15, Appl | | |
| 10 | 517.2 | 48.5 | 860 | 5 | US-10-244-779-1 | Sequence 1, Appl | | |
| 11 | 507.4 | 47.6 | 729 | 9 | US-10-851-636-12 | Sequence 12, Appl | | |
| 12 | 507.2 | 47.6 | 678 | 9 | US-10-851-636-4 | Sequence 4, Appl | | |
| 13 | 497.8 | 46.7 | 729 | 9 | US-10-851-636-13 | Sequence 13, Appl | | |
| 14 | 497.4 | 46.7 | 678 | 9 | US-10-851-636-5 | Sequence 5, Appli | | |
| 15 | 486.4 | 45.6 | 678 | 9 | US-10-492-081B-2 | Sequence 2, Appli | | |
| 16 | 467.2 | 43.8 | 675 | 9 | US-10-851-636-3 | Sequence 3, Appl | | |
| 17 | 467.2 | 43.8 | 726 | 6 | US-10-851-636-11 | Sequence 11, Appl | | |
| 18 | 465 | 43.6 | 726 | 6 | US-10-314-827-3 | Sequence 3, Appl | | |
| 19 | 461.8 | 43.3 | 726 | 6 | US-10-314-827-5 | Sequence 5, Appl | | |
| 20 | 460.2 | 43.2 | 726 | 6 | US-10-314-827-13 | Sequence 13, Appl | | |
| 21 | 458.6 | 43.0 | 726 | 6 | US-10-314-827-11 | Sequence 11, Appl | | |
| 22 | 457 | 42.9 | 726 | 6 | US-10-314-827-9 | Sequence 9, Appli | | |
| 23 | 455.4 | 42.7 | 726 | 6 | US-10-314-827-7 | Sequence 7, Appli | | |
| 24 | 436 | 40.9 | 745 | 6 | US-10-314-827-17 | Sequence 17, Appl | | |
| 25 | 436 | 40.9 | 746 | 6 | US-10-314-827-15 | Sequence 15, Appl | | |
| 26 | 433 | 40.6 | 748 | 6 | US-10-314-827-19 | Sequence 19, Appl | | |
| 27 | 432.8 | 40.6 | 684 | 7 | US-10-664-341-68 | Sequence 68, Appl | | |
| 28 | 431.6 | 40.5 | 681 | 6 | US-10-314-827-1 | Sequence 1, Appli | | |
| 29 | 419.6 | 39.4 | 801 | 3 | US-09-967-772-7 | Sequence 7, Appli | | |
| 30 | 419.6 | 39.4 | 801 | 6 | US-10-335-517-7 | Sequence 7, Appl | | |
| 31 | 419.6 | 39.4 | 801 | 6 | US-10-334-288-7 | Sequence 7, Appli | | |
| 32 | 419.6 | 39.4 | 801 | 8 | US-10-311-030-6 | Sequence 6, Appli | | |
| 33 | 419.6 | 39.4 | 801 | 5 | US-10-656-029-23 | Sequence 23, Appl | | |
| 34 | 419.6 | 39.4 | 1116 | 8 | US-10-006-922-3 | Sequence 3, Appl | | |
| 35 | 418.6 | 39.3 | 845 | 8 | US-10-757-356-3 | Sequence 3, Appl | | |
| 36 | 409.2 | 38.4 | 741 | 9 | US-10-851-636-14 | Sequence 14, Appl | | |
| 37 | 405.4 | 38.0 | 693 | 9 | US-10-851-636-6 | Sequence 6, Appli | | |
| 38 | 380 | 35.6 | 725 | 9 | US-10-851-636-39 | Sequence 39, Appl | | |
| 39 | 380 | 35.6 | 726 | 9 | US-10-851-636-38 | Sequence 38, Appl | | |
| 40 | 380 | 35.6 | 726 | 9 | US-10-851-636-43 | Sequence 43, Appl | | |
| 41 | 378.4 | 35.5 | 725 | 9 | US-10-851-636-41 | Sequence 41, Appl | | |
| 42 | 378.4 | 35.5 | 726 | 9 | US-10-851-636-40 | Sequence 40, Appl | | |
| 43 | 378.4 | 35.5 | 726 | 9 | US-10-851-636-44 | Sequence 44, Appl | | |
| 44 | 375.2 | 35.2 | 726 | 9 | US-10-851-636-42 | Sequence 42, Appl | | |
| 45 | 371.8 | 34.9 | 680 | 9 | US-10-851-636-91 | Sequence 91, Appl | | |

## ALIGNMENTS

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RESULT 1
US-10-757-356-17
; Sequence 17, Application US/1075356
; Publication No. US20050032085A1
; GENERAL INFORMATION:
;   APPLICANT: Labas, Yulii Aleksandrovich
;   APPLICANT: Gurskaya, Nadezda Georgievna
;   APPLICANT: Yanushevich, Yuriy
;   APPLICANT: Fradkov, Arcady Fedorovich
;   APPLICANT: Lukyanov, Konstantin
;   APPLICANT: Lukyanov, Sergey
;   APPLICANT: Matz, Mikhail Vladimirovich
;   TITLE OF INVENTION: NOVEL CHROMOPHORES/FLUOROPHORES AND
;   TITLE OF INVENTION: METHODS FOR USING THE SAME
;   FILE REFERENCE: CLON-090
;   CURRENT APPLICATION NUMBER: US/10/757,356
;   CURRENT FILING DATE: 2004-01-13
;   PRIOR APPLICATION NUMBER: 60/332,980
;   PRIOR FILING DATE: 2001-11-13
;   PRIOR APPLICATION NUMBER: PCT/US02/36499
;   PRIOR FILING DATE: 2002-11-12
;   NUMBER OF SEQ ID NOS: 28
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
;   LENGTH: 1066
;   TYPE: DNA
;   ORGANISM: Montastraea cavernosa
US-10-757-356-17

  Query Match             100.0%;  Score 1066;  DB 8;  Length 1066;
  Best Local Similarity   100.0%;  Pred. No. 1e-310;
  Matches 1066;  Conservative . 0;  Mismatches 0;  Indels 0;  Gaps 0;

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Qy         61 TCTTACTTACGTCTACCATCATGACAAGTGTTGCACAGGAAAAGGGGTGTGATTAAACCAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCTTACTTACGTCTACCATCATGACAAGTGTTGCACAGGAAAAGGGGTGTGATTAAACCAG 120

Qy        121 ACATGAAGATGAAGCTGCGTATGGAAGGTGCTGTAAACGGGCACAAGTTCGTGGTTGAAG 180
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Db        121 ACATGAAGATGAAGCTGCGTATGGAAGGTGCTGTAAACGGGCACAAGTTCGTGGTTGAAG 180

Qy        181 GAGATGGAAAAGGGAAGGCTTTCGACGGAACACAGACTATGGACCTTACAGTCATAGAAG 240
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TITLE OF INVENTION: METHODS FOR USING THE SAME
; FILE REFERENCE: CLON-090
; CURRENT APPLICATION NUMBER: US/10/757,356
; CURRENT FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: 60/332,980
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: PCT/US02/36499
; PRIOR FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 913
; TYPE: DNA
; ORGANISM: Montastraea cavernosa
US-10-757-356-25

Query Match   78.7%;   Score 838.8; DB 8;   Length 913;
Best Local Similarity 96.9%; Pred. No. 4e-242;
Matches 866; Conservative 0; Mismatches 27; Indels 1; Gaps 1;

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Db     9 AGGGTGATATCTTACTTACGTCTCCACCATCATGACACCAGTGTTGCACAGGAAAAGGGTGTGA 68

Qy   112 TTAAACCAGACATGAAGATGAAGCTGGTATGGAAGTGCTGTAAACGGGCACAAGTTCG 171
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Db    69 TTAAACCAGACATGAAGATGAAGCTGCGTATGGAAGTGCTGTAAACGGGCACAAGTTCG 128

Qy   172 TGGTTGAAGGAGGATGGAAAAGGGAAGCCTTTCGACGGAACACAGACTTTCGACGACCTTACAG 231
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Db   129 TGATTGAAGGAGGATGGAAAAGGGAAGCCTTTCGACGGAACACAGACATG GACCTTACAG 188

Qy   232 TCATAGAAGGGCCACCATTGCCTTCGCTTACGATATCTTGACAACAGTATTCGATTACG 291
         |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db   189 TCATAGAAGGGCCACCATTGCCTTCGCTTACGATATCTTGACAACAGTATTCGATTACG 248

Qy   292 GCAACAGGGTATTCGCCAAATACCCAGAAGACATAGCACAGATTATTTCAAGCAGACGTTTC 351
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   249 GCAACAGGGTATTCGCCAAATACCCAGAAGACATAGCACAGATTATTTCAAGCAGACATTTC 308

Qy   352 CTGAGGGGTACTTCTGGAACGAAGCATGACATACGAAGACGAAGACCAGGGCATTTGCATCGCCA 411
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   309 CTGAGGGGTACTTCTGGAACGAAGCATGACATACGAAGACGAAGACCAGGGCATTTGCATCGCCA 368

Qy   412 CAAACGACATAACAATGATGAAGGCGTCGACGACTGTTTGCCTATAAAATTCGATTTG 471
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   369 CAAACGACATAACAATGATGAAGGCGTCGACGACTGTTTGCCTATAAAATTCGATTTG 428

Qy   472 ATGGTGTGAACTTTCCTGCCAATGGTCCAGTTATGCGAGGAAGACGCTGAAATGGGAGC 531
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   429 ATGGTGTGAACTTTCCTGCCAATGGTCCAGTTATGCGAGGAAGACGCTGAAATGGGAGC 488

Qy   532 CATCCACTGAGATAATGTATGCGCGTGATGAGTGCGTGAAGGGTGATGTTAACATGGCTC 591
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   489 CATCCACTGAGAAAATGTATGCGCGTGATGAGTGCGTGAAGGGTGATGTTAACATGGCTC 548

Qy   592 TGTTGCTTGAAGGAGGTGGCCATTACCGATGTGACTTCAAAACTACTTACAAAGCTAAGA 651
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   549 TGTTGCTTGAAGGAGGTGGCCATTACCGATGTGACTTCAAAACTACTTACAAAGCTAAGA 608

Qy   652 AGGTTGTCCGGTTGCCAGACTATCACTTGTGACCATCGCATTGAGATTGTGAGCCACG 711
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   609 AGGTTGTCCGGTTGCCAGACTATCATCATTTGTGACCATCGCATTGAGATTGTGAGCCACG 668

Qy   712 ACAAAGATTACAACAAGTTAAGCTGCACGAGCATGCCGAAGCTCGTCATGGACTGTCAA 771
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   669 ACAAAGATTACAACAAGTTAAGCTGTATGAGCATGCCGAAGCTCATTCTGGGCGTGCCGA 728

Qy   772 GGAAGGCCAAGTAAAAGGCTTAATGAAAAGTCAAGACGAACAACGAGGAGAAAACAAAGTA-C 830
         |||||||||||||||||||||||||||||||||||||||||
Db   729 GGCAGGCCAAGTAAAAGGCTTAATGAAAAGCCAAGAACAACGAGGAGAAAACAAAGTATT 788

Qy   831 TTTTTGTTAAATTGAAGGCATTACTCGGAATTAGTATTGATATCTTTCGATTCAAGG 890
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; RESULT 2
; US-10-757-356-25
; Sequence 25, Application US/10757356
; Publication No. US20050032085A1
; GENERAL INFORMATION:
; APPLICANT: Labas, Yulii Aleksandrovich
; APPLICANT: Gurskaya, Nadezda Georgievna
; APPLICANT: Yanushevich, Yuriy
; APPLICANT: Fradkov, Arcady Fedorovich
; APPLICANT: Lukyanov, Konstantin
; APPLICANT: Lukyanov, Sergey
; APPLICANT: Matz, Mikhail Vladimirovich
; TITLE OF INVENTION: NOVEL CHROMOPHORES/FLUOROPHORES AND

```
Db   181 GAGATGCAGAAAGGAAGCCTTTCGACGGCAACAGACTATGACCTTACAGTCATAGAAG 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   241 GCGCACCATTGCCTTCGCTTACGATATCTTGCACAACAGTATTCGATTACGGCCAACAGGG 300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 GCGCACCATTGCCTTCGCTTACGATATCTTGCTACAACAGTATTCGATTACGGCCAACAGGG 300

Qy   301 TATTCGCCAAATACCCAGAAGACATAGCACAGATTATTTCAAGCAGACAGCGTTTCCTGAGGGGT 360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 TATTCGCCAAATACCCAGAAGACATAGCACAGATTATTTCAAGCAGACAGCGTTTCCTGAGGGGT 360

Qy   361 ACTTCTGGAACGAAGCATGACATACGAAGACCAGGGCATTTGCATCGCCACAAACGACA 420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 ACTTCTGGAACGAAGCATGACATACGAAGACCAGGGCATTTGCATCGCCACAAACGACA 420

Qy   421 TAACAATGATGAAGGCGGTCGACGACTGTTTGCCTATAAAATTCGATTTGATGGTGTGA 480
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 TAACAATGATGAAGGCGGTCGACGACTGTTTGCCTATAAAATTCGATTTGATGGTGTGA 480

Qy   481 ACTTTCCTGCCAATGTCCAGTTATGCGAGGAAGACGCTGAAATGGGAGCCATCCACTG 540
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 ACTTTCCTGCCAATGGTCCAGTTATGCGAGGAAGACGCTGAAATGGGAGCCATCCACTG 540

Qy   541 AGATAATGTATGCGCGTGATGAGTGCGTGAAGGGTGATGTGTTAACATGGCTCTGTTGCTTG 600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 AGATAATGTATGCGCGTGATGAGTGCGTGAAGGGTGATGTGTTAACATGGCTCTGTTGCTTG 600

Qy   601 AAGGAGGTGGCCATTACCGATGTGACTTCAAAACTACTTACAAAGCTAAGAAGGTGTCC 660
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 AAGGAGGTGGCCATTACCGATGTGACTTCAAAACTACTTACAAAGCTAAGAAGGTGTCC 660

Qy   661 GGTTGCCAGACTATCACTTGTGGACCATCGCATTGAGATTGTGAGCCACGACAAAGATT 720
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 GGTTGCCAGACTATCACTTGTGGACCATCGCATTGAGATTGTGAGCCACGACAAAGATT 720

Qy   721 ACAACAAGTTAAGCTGCACGAGCATGCCGAAGCTCGTCATGGACTGTCAAGGAAGGCCA 780
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 ACAACAAGTTAAGCTGCACGAGCATGCCGAAGCTCGTCATGGACTGTCAAGGAAGGCCA 780

Qy   781 AGTAAAAGGCTTAATGAAAAGTCAAGACGAACAACGAGGAGAAAACAAAGTACTTTTTGTTA 840
         ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db   781 AGTAAAAGGCTTAATGAAAAGTCAAGACGAACAACGAGGAGAAAACAAAGTACTTTTTGTTA 840

Qy   841 AATTTGAAGGCATTACTCGGAATTAGTATTGATACTTTCGATTCAAGGATTTGTTCCG 900
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 AATTTGAAGGCATTACTCGGAATTAGTATTGATACTTTCGATTCAAGGATTTGTTCCG 900

Qy   901 GGATTGTTAGAGACTAGCTCTAGAGTTGTATTTTGTGAAAAAAGATAGTTTCCAGTTTT 960
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 GGATTGTTAGAGACTAGCTCTAGAGTTGTATTTTGTGAAAAAAGATAGTTTCCAGTTTT 960

Qy   961 TGCGGGATTACAGCATGGGGATAGACTTTTTAAACTCAGTTGTGCTCAAGTAAG 1020
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 TGCGGGATTACAGCATGGGGATAGACTTTTTAAACTCAGTTGTGGTCAAGTAAG 1020

Qy  1021 AAAACTGTAGTGAGAATAAACTTGTTATCGGAAGCCGAAAAAAAAAA 1066
         |||||||||||||||||||||||||||||||||||||
Db  1021 AAAACTGTAGTGAGAATAAACTTGTTATCGGAAGCCGAAAAAAAAAA 1066
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Db   789 ||||||||||| |||||||||||||||||||||||||||||||||||||||||||||| 848
             TTTTTGTTAAATTCAAGGCATTAGTTACTCGGAATTAGTATTTGTATCTTTCGATTCAAGG

Qy   891 ATTTGTTCCGGGATTTGTTAGAGACTAGCTCTAGAGTTGTATTTTGTGAAAAA 944
             |||||| ||| |||||||||||||||||||||||||||||||||||||||||
Db   849 ATTTGTTTCGGGACTTGTTAGAGACCAGCTCTAGAGTCGTAGAGTTGTGAAAAA 902

RESULT 3
US-10-757-356-27
; Sequence 27, Application US/10757356
; Publication No.US20050012085A1
; GENERAL INFORMATION:
;   APPLICANT: Labas, Yulii Aleksandrovich
;   APPLICANT: Gurskaya, Nadezda Georgievna
;   APPLICANT: Yanushevich, Yuriy
;   APPLICANT: Fradkov, Arcady Fedorovich
;   APPLICANT: Lukyanov, Konstantin
;   APPLICANT: Lukyanov, Sergey
;   APPLICANT: Matz, Mikhail Vladimirovich
;   TITLE OF INVENTION: NOVEL CHROMOPHORES/FLUOROPHORES AND
;   TITLE OF INVENTION: METHODS FOR USING THE SAME
;   FILE REFERENCE: CLON-090
;   CURRENT APPLICATION NUMBER: US/10/757,356
;   CURRENT FILING DATE: 2004-01-13
;   PRIOR APPLICATION NUMBER: 60/332,980
;   PRIOR FILING DATE: 2001-11-13
;   PRIOR APPLICATION NUMBER: PCT/US02/36499
;   PRIOR FILING DATE: 2002-11-12
;   NUMBER OF SEQ ID NOS: 28
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 27
;   LENGTH: 1133
;   TYPE: DNA
;   ORGANISM: Montastraea annularis
US-10-757-356-27

  Query Match   62.4%; Score 665; DB 8; Length 1133;
  Best Local Similarity   80.4%; Pred. No. 1.5e-189;
  Matches 855; Conservative   2; Mismatches 162; Indels 44; Gaps 5;

Qy   1 ATTTCGCCCTGGTGATTTCGAAGAGAGCAGATCGAGAACAACAAGAGCTGTA--AGTTGA   58
             ||||||| |||| |||||||||||||| | ||||| |||||||||||| ||||| ||||||
Db   99 ATTCACCCTGGTGATTTGGAAGAGAGCAGATCGAGAACACCAAGAGCTGTATTACGCTAA 158

Qy   59 TATCTTACTTACGTCTCACCATCATGACAAGTGTTGCACAGGAAAAGGTGTGATTAAACC 118
             |||||||||||||| |||||| |||||||||| ||||||||||||||||
Db   159 AATCTTACTTACGTGCCTCTACACCACCATGA------------GTATGATTAAACC 197

Qy   119 AGACATGAAGATGAAGCTGCGTATGGAAGGTGCTGTAAACGGGCACAAGTTCGTGGTTGA 178
             ||| ||||||||||||| | ||||||| || |||||||||||||| |||||||||
Db   198 AGAAATGAAGATCAAGATGCGTATGGACGGTGCGTGTAAACGGCACAAGTTCGTGATTAC 257

Qy   179 AGGAGATGGGAAAAGGGAGAGCCTTTGCACGGACCGGACCACAGACGAGATGGACCATCATCAGA 238
             ||||||| ||||||| ||| || |||||||||| ||||||||| |||||||| ||||||
Db   258 AGGGGAAGGAAGCGGCGAGCCTTTGCAGACGCCTTTGCGACGGGACCAGACCATGATCAGACAGTCA 317

Qy   239 AGGCGCACCATTGCCCTTTCGCTTACGATATCTTGACAACAGTATTCGATTACGGCAACAG 298
             ||||||||||| |||| ||||||||||| | ||||||||||||| ||||||| |||
Db   318 CGGCGGCACCCTCTGCCCTTTCGCTTTCGCAATCATCTTGACAACAGCATTCGATTACGGCAGCAMCAG 377

Qy   299 GGTATTCGCCAAATACCCAGAAGCATAGCAGATTATTCAAGCAGCAGACGCTTCCTGAGGG 358
             ||||||||||||||||||||||| || ||||||||| ||||||| |||||||||| ||
Db   378 GGTATTCGCCAAATACCCAGAACGATCCCAGACTATTTCAAGCAGTCGTTTTCGTTTCCTGAGGG 437

Qy   359 GTACTTCTGGGAACGAAGCGATGACCATGACATAGGACGACCAGGGCATTTGCATCGGCCACAAACGA 418
             ||||| || ||||| |||||||||||||||| ||||||| ||||||||||||||| ||||||
Db   438 GTTTTTCTTGGGAACGAAGCAGTGACGACTTACGAAGAACGACGGGGCATTTGCATCGCGCCACAAATGA 497

Qy   419 CATAACAATGATGATGAAGGCGTCGACAGCTGTTTTGCCTATAAAATTCGATTGATGTGT 478
             ||| ||| ||||||| |||||| |||||||||| ||| ||
Db   498 CATAAAAATG------GAAGGCGACTGCTTTTTCCTATGAAATTCGATTGATGTGGGT 548

Left column:

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Qy   102 AAGGGTGTGATTAAACCAGACATGAAGATGAAGCTGCGTATGGAAGGTGCTGTAAACGGG 161
             || ||||| |||||||||||||||||||||| ||||||||||||||||||||||||||
Db     1 ATGAGTGTGATAAAACCAGACATGAAGATGAAGATCAAGCTGCGTATGGAAGGTGCTGTAAACGGG 60

Qy   162 CACAAGTTCGTGGTTGAAGGAGATGGAAAGGCAGCCTTTCGACGGAAACAGACTATG 221
          |||||||||||| |||||||||||||||||| |||||||||||||||||||||||||
Db    61 CACAAGTTCGTGATTCGATTGAAGGAGACATAGCGACCTTTCGCCTTTACGATATCTTGACAACAGTA 120

Qy   222 GACCTTACAGTCATAGAAGCACAGGGGTATTCGCCAAATACCCAGAAGACATAGAAGACCAGGGCAT 281
          ||||||||||||||||||||||||| ||||| ||||||||||||||||||||||||||||||| |
Db   121 GACCTTACAGTCATAGAAGCGCAACCTTTCGCCTTTACGATATCTTGACAACAGTA 180

Qy   282 TTCGATTACGGCAACAGGGGTACTTCTGGGAACGATGATGAAGACATAGACAAGAGAGACGCATT 341
          |||||||||||||||||| |||||||||||||||||||||||||||||||| |||||||||||
Db   181 TTCGATTACGGCAACAGGGGTACTCCTGGGAACGAACGAAGCATGATGAACAATACCAGAAGACATAGAAG 240

Qy   342 CAGACGTTTCCTGAGGGGTACTTCTGGGAACGAACGAAGCATGATGAACAATACCAGAAGACGCTG 401
          ||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db   241 CAGACGTTTCCGGAGGGGTACTCCTGGGAACGAACGAAGCATGATGAACAATACCAGAAGACGCATT 300

Qy   402 TGCATCGCCACAAACGACATAACAATGATGAAGGCGTCGACGACTGTTTTGTCTATAAA 461
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 TGCATCGCCACAAACGACATAACAATGATGAAGGCGTCGACGACTGTTTTGTCTATAAA 360

Qy   462 ATTCGATTTGATGGTGTGAACTTTCCTGCCAATGTGCGCGTGATGGAGTGCTGAAGGGTGATGTT 521
          |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db   361 ATTCGATTTGATGGTGTGAACTTTCCTGCCAATGTGCGCGTGATGGAGTGCTGAAGGGTGATGTT 420

Qy   522 AAATGGAGCCATCCACTGAGATAATGTATGCGCGTGATGGGGTACTGAAGGGTGATGTT 581
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 AAATGGGGAGCCATCCACTGAGATAATGTATGCGCGTGATGGGGTACTGAAGGGTGATGTT 480

Qy   582 AACATGGCTCTGTTGCTTGAAGGAGTGGCCATTACCGATGTGACTTCAAAACTACTTAC 641
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 AACATGGCTCTGTTGCTTGAAGGAGTGGCCATTACCGATGTGACTTCAAAACTACTTAC 540

Qy   642 AAAGCTAAGAAGGTTGTCCGGTTGCCGGTTGCCAGACTATCACTTTGTTGCCATGCCATTGGAGATT 701
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 AAAGCTAAGAAGGTTGTCCAGTTGCCAGACTATCATTTTGTTGCCATGCCATTGGAGATT 600

Qy   702 GTGAGCCACGACAAAGATTACAACAAGGTTAAGCTGTATGAGCTCGTCAT 761
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GTGAGCCACCAGCAAAGATTACAACAAGGTTAAGCTGTATGAGCTCATTCT 660

Qy   762 GGACTGTCAAGGAAGGCCAAGTAA 785
          ||||||||| || ||||||||||||
Db   661 GGGCTGCCGAGGCAGGCCAAGTAA 684
```

RESULT 5
US-10-314-936-7
; Sequence 7, Application US/10314936
; Publication No. US2004011225A1
; GENERAL INFORMATION:
; APPLICANT: Gibbs, Patrick D.L.
; APPLICANT: Carter, Robert W.
; APPLICANT: Schmale, Michael C.
; TITLE OF INVENTION: FLUORESCENT PROTEINS FROM AQUATIC SPECIES
; FILE REFERENCE: 638.004
; CURRENT APPLICATION NUMBER: US/10/314,936
; CURRENT FILING DATE: 2002-12-09
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 684
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: mutant green fluorescent protein
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(684)
; OTHER INFORMATION:

Right column:

US-10-314-936-7

Query Match   58.9%; Score 628; DB 7; Length 684;
Best Local Similarity 94.9%;   Pred. No. 1.7e-178;
Matches 649; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

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Qy   102 AAGGGTGTGATTAAACCAGACATGAAGATGAAGCTGCGTATGGAAGGTGCTGTAAACGGG 161
             || ||||| |||||||||||||||||||||| ||||||||||||||||||||||||||
Db     1 ATGAGTGTGATAAAACCAGACATGAAGATGAAGATCAAGCTGCGTATGGAAGGTGCTGTAAACGGG 60

Qy   162 CACAAGTTCGTGGTTGAAGGAGATGGAAAGGCAGCCTTTCGACGGAAACAGACTATG 221
          |||||||||||| |||||||||||||||||| |||||||||||||||||||||||||
Db    61 CACAAGTTCGTGATTCGATTGAAGGAGACGGCAGCCTTTCGCCTTTACGATATCTTGACAACAGTA 120

Qy   222 GACCTTACAGTCATAGAAGCACAGGGCGCCACCTTTCGCCTTTACGATATCTTGACAACAGTA 281
          |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db   121 GACCTTACAGTCATAGAAGCGCAACCGCACCTTTCGCCTTTACGATATCTTGACAACAGTA 180

Qy   282 TTCGATTACGGCAACAGGGGTATTCGCCAAATACCCAGAAGACATAGCAGATTATTTCAAG 341
          |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db   181 TTCGATTACGGCAACAGGGGTATTCGCCAAATACCCAATACCAGAAGACATACCAGAAGATTATTTCAAG 240

Qy   342 CAGACGTTTCCTGAGGGGTACTTCTGGGAACGATGACATGACATACGAAGACCAGGGCATT 401
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 CAGACGTTTCCGGAGGGGTACTCCTGGGAACGATGACATGACATACGAAGACCAGGGCATT 300

Qy   402 TGCATCGCCACAAACGACATAACAATGATGGAAGCGTCGACGACTGTTTTGTCTATAAA 461
          ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db   301 TGCATCGCCACAAACGACATAACAATGATGAAGCGTCGACGACTGTTTTGTCTATAAA 360

Qy   462 ATTCGATTTGATGGTGTGAACTTTCCTGCCAATGTGCGCGTGATGGAGTGCTGAAGGGTGATGTT 521
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 ATTCGATTTGATGGTGTGAACTTTCCTGCCAATGTGCGCGTGATGGAGTGCTGAAGGGTGATGTT 420

Qy   522 AAATGGAGCCATCCACTGAGATAATGTATGCGCGTGATGGGGTACTGAAGGGTGATGTT 581
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 AAATGGGGAGCCATCCACTGAGAAAAATGTATGTGCGTGATGGGTACTGAAGGGTGATGTT 480

Qy   582 AACATGGCTCTGTTGCTTGAAGGAGTGGCCATTACCGATGTGACTTCAAAACTACTTAC 641
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 AACATGGCTCTGTTGCTTGAAGGAGTGGCCATTACCGATGTGACTTCAAAACTACTTAC 540

Qy   642 AAAGCTAAGAAGGTTGTCCGGTTGCCGGTTGTCCGGTTGCCAGACTATCACTTTGTTGCCATGCCATTGAGATT 701
          ||||||||||||||||| |||||||||||||||||||||||||||||||||
Db   541 AAAGCTAAGAAGGTTGTCCAGTTGTCCAGTTGCCAGACTATCATTTTGTTGCCATGCCATTGAGATT 600

Qy   702 GTGAGCCACGACAAAGATTACAACAAGGTTAAGCTGTATGAGCTCGTCAT 761
          ||||||||| |||||||||||||||||||||||||||||||||||||||
Db   601 GTGAGCCACCAGCAAAGATTACAACAAGGTTAAGCTGTATGAGCTCATTCT 660

Qy   762 GGACTGTCAAGGAAGGCCAAGTAA 785
          ||||||||| || |||||||||||
Db   661 GGGCTGCCGAGGCAGGCCAAGTAA 684
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RESULT 6
US-11-021-014-7
; Sequence 7, Application US/11021014
; Publication No. US2005010954A1
; GENERAL INFORMATION:
; APPLICANT: Gibbs, Patrick D.L.
; APPLICANT: Carter, Robert W.
; APPLICANT: Schmale, Michael C.
; TITLE OF INVENTION: FLUORESCENT PROTEINS FROM AQUATIC SPECIES
; FILE REFERENCE: 638.004
; CURRENT APPLICATION NUMBER: US/11/021,014
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: US/10/314,936
; PRIOR FILING DATE: 2002-12-09
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 684

```
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: mutant green fluorescent protein
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(684)
;   OTHER INFORMATION:
US-11-021-014-7

Query Match     58.9%;  Score 628;  DB 10;  Length 684;
Best Local Similarity  94.9%;  Pred. No. 1.7e-178;
Matches  649;  Conservative  0;  Mismatches  35;  Indels  0;  Gaps  0;

Qy  102 AAGGGTGTGATTAAACCAGAACATGAAGATGAAGTGCGTATGGAAGGTGCTGTAAACGGG 161
            | ||||||| |||||||||||||||||||| |||||||||||||||||||||||||||
Db    1 ATGAGTGTGATAAAACCAGAACATGAAGATCAAGTGCGTATGGAAGGTGCTGTAAACGGG 60

Qy  162 CACAAGTTCGTGGTTGAAGGAGACGGCGCACCATTGCCTTTCGCTTACGATATCTTGACAACAGTA 221
            ||||||||||||| |||||||||||||||||||||||||||||| ||||||||||||||
Db   61 CACAAGTTCACAGAAGGGGTGTATTCGCCAAATACCCAGAAGACATGACATAGCGCATT 120

Qy  222 GACCTTACAGTCATAGAGAGGCGCACCATTGCCTTTCGCTTACGATATCTTGACAACAGTA 281
            |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db  121 GACCTTACAGTCATAGAAGCATACCAAATACCCAGAAGACATGACATAGCGCATT 180

Qy  282 TTCGATTACGGCAACAGGTGTACTTCTGGGAACGAAGCATGACATAGCGCATT 341
            |||||||||||||||||||||||||||||||||||||||||||||| |||||
Db  181 TTCGATTACGGCAACAGGTGTATTCGCCAAATACCCAGAAGACATGACATAGCGCATT 240

Qy  342 CAGACGTTTCCTGAGGGGTACTTCTGGGAACGAAGCATGACATAGCGCATT 401
            |||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 CAGACGTTTCCGGAGGGGGTACTTCTGGGAACGAAGCATGACATAGCGCATT 300

Qy  402 TGCATCGCCACAAACGACATAACAATGATGGAAGGCGTCGACGACTGTTTTGCCTATAAA 461
            |||||||||||||||||||||||||||||||||||| |||||||||||||| ||||||
Db  301 TGCATCGCCACAAACGACATAACAATGATGAAAGGCGTCGACGTGTTTGTCTATAAA 360

Qy  462 ATTCGATTTGATGGTGTGAACTTCCTGCCAATGGTCGCGTGATTACCGATGTGATGTT 521
            ||||||||||||||||||||||||||||||| |||||||||||| |||||||||||
Db  361 ATTCGATTTGATGGTGTGAACTTCCTGCCAATGGTCCAGTTATGCAGAGGAAGACGCTA 420

Qy  522 AAATGGGAGCCATCCACTGAGATAATGTATGCGCGTGATGGAGTGCTGAAGGGTGATGTT 581
            ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db  421 AAATGGGAGCCATCCACTACCGATGTGACTTCAAAACTACTTAC 480

Qy  582 AACATGGCTCGTGTTGCTTGAAGGAGGTGGCCATTACCGATGTGACTTCAAAACTACTTAC 641
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 AACATGGCTCGTGTTGCTTGAAGGAGGTGGCCATTACCGATGTGACTTCAAAACTACTTAC 540

Qy  642 AAAGCTAAGAAGGTGTCCGGTTGCCGAGCATCACTTTGTTGACCATGCGATTGAGATT 701
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541 AAAGCTAAGAAGGTGTCCGGTTGCCGAGCATCACTTTGTTGACCATGCGATTGAGATT 600

Qy  702 GTGAGCCACGACAAAGATTACAACAAGTTAAGCTGCACGGAGCATGCCGAGCTCGTCAT 761
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601 GTGAGCCACGACAAAGATTACAACAAGTTAAGCTGTATGAGCATGCCGAGCTCATTCT 660

Qy  762 GGACTGTCAAGGAAGGCCAAGTAA 785
            |||| |||  || ||||||||||
Db  661 GGGCTGCCGAGGCAGGCCAAGTAA 684
```

RESULT 7
US-10-314-936-5
; Sequence 5, Application US/10314936
; Publication No. US20040110225A1
; GENERAL INFORMATION:
; APPLICANT: Gibbs, Patrick D.L.
; APPLICANT: Carter, Robert W.
; APPLICANT: Schmale, Michael C.
; TITLE OF INVENTION: FLUORESCENT PROTEINS FROM AQUATIC SPECIES
; FILE REFERENCE: 638.004

```
;   CURRENT APPLICATION NUMBER: US/10/314,936
;   CURRENT FILING DATE: 2002-12-09
;   NUMBER OF SEQ ID NOS: 15
;   SOFTWARE: PatentIn version 3.1
;   SEQ ID NO 5
;     LENGTH: 684
;     TYPE: DNA
;     ORGANISM: Artificial
;     FEATURE:
;     OTHER INFORMATION: mutant green fluorescent protein
;     FEATURE:
;     NAME/KEY: CDS
;     LOCATION: (1)..(684)
;     OTHER INFORMATION:
US-10-314-936-5

Query Match     58.8%;  Score 626.4;  DB 7;  Length 684;
Best Local Similarity  94.7%;  Pred. No. 5.1e-178;
Matches  648;  Conservative  0;  Mismatches  36;  Indels  0;  Gaps  0;

Qy  102 AAGGGTGTGATTAAACCAGAACATGAAGATGAAGTGCGTATGGAAGGTGCTGTAAACGGG 161
            | ||||||| |||||||||||||||||||| |||||||||||||||||||||||||||
Db    1 ATGAGTGTGATAAAACCAGAACATGAAGATCAAGTGCGTATGGAAGGTGCTGTAAACGGG 60

Qy  162 CACAAGTTCGTGATTGAAGGAGACGGCGCACCATTGCCTTTCGACGGAACACAGACTATG 221
            |||||||||||||||||||||||||||||||||||||||||||| |||| |||||||||
Db   61 CACAAGTTCGTGATTGAAGGAGACGGCGCACCTTTGCCTTTCGACGGAAAAACAGACTATG 120

Qy  222 GACTTACAGTCATAGAGAGGCGCACCATTGCCTTTCGCTTACGATATCTTGACAACAGTA 281
            ||||||||||||||||||| |||||| ||||||||||||||||||||||||||||||||
Db  121 GACTTACAGTCATAGAACGGCGCACCTTTGCCTTTCGCTTACGATATCTTGACAACAGTA 180

Qy  282 TTCGATTACGGCAACAGGTGTATTCGCCAAATACCCAGAAGACATTATTCAAG 341
            ||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db  181 TTCGATTACGGCAACAGGTGTATTCGCCAAATACCCAGAAGACTATTTCAAG 240

Qy  342 CAGACGTTTCCTGAGGGGTACTTCTGGGAACGACATACGAAGACCAGGGCATT 401
            |||||||||||||||||||||||||||||||| |||||||||||||||||||
Db  241 CAGACGTTTCCGGAGGGGTACTTCTGGGAACGACATACGAAGACCAGGGCATT 300

Qy  402 TGCATCGCCACAAACGACATAACAATGATGGAAGGCGTCGACGACTGTTTTGCCTATAAA 461
            ||||||||||||||||||||||||||||||||||| |||||||||||||| ||||||
Db  301 TGCATCGCCACAAACGACATAACAATGATGAAAGGCGTCGACGTGTTTGTCTATAAA 360

Qy  462 ATTCGATTTGATGGTGTGAACTTCCTGCCAATGGTCGCGTATGCAGAGGAAGACGCTG 521
            ||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db  361 ATTCGATTTGATGGTGTGAACTTCCTGCCAATGGTCCAGTTATGCAGAGGAAGACGCTA 420

Qy  522 AAATGGGAGCCATCCACTCCACTGTGCCGTGATAATGTATGCGCGTGATGGGGTGATGTT 581
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 AAATGGGAGCCATCCACTCCACTGTGCCGTGATAATGTATGCGCGTGATGGGGTGATGTT 480

Qy  582 AACATGGCTCGTGTTGCTTGAAGGAGGTGGCCATTACCGATGTGACTTCAAAACTACTTAC 641
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 AACATGGCTCGTGTTGCTTGAAGGAGGTGGCCATTACCGATGTGACTTCAAAACTACTTAC 540

Qy  642 AACGCTAAGAAGGTGTCCGGTTGCCGAGCATCACTTTGTTGACCATGCGATTGAGATT 701
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541 AACGCTAAGAAGGTGTCCGGTTGCCGAGCATCACTTTGTTGACCATGCGATTGAGATT 600

Qy  702 GTGAGCCACGACAAAGATTACAACAAGGTGTCCAGTTGCCGAGCATGCCGAGCTCGTCAT 761
            |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db  601 GTGAGCCACGACAAAGATTACAACAAGTTAAGCTGTATGAGCATGCCGAGCTCATTCT 660

Qy  762 GGACTGTCAAGGAAGGCCAAGTAA 785
            |||| |||  || ||||||||||
Db  661 GGGCTGCCGAGGCAGGCCAAGTAA 684
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RESULT 8
US-11-021-014-5
; Sequence 5, Application US/11021014
; Publication No. US20050100954A1
```

; GENERAL INFORMATION:
;   APPLICANT: Gibbs, Patrick D.L.
;   APPLICANT: Carter, Robert W.
;   APPLICANT: Schmale, Michael C.
;   TITLE OF INVENTION: FLUORESCENT PROTEINS FROM AQUATIC SPECIES
;   FILE REFERENCE: 638.004
;   CURRENT APPLICATION NUMBER: US/11/021,014
;   CURRENT FILING DATE: 2004-12-23
;   PRIOR APPLICATION NUMBER: US/10/314,936
;   PRIOR FILING DATE: 2002-12-09
;   SOFTWARE: PatentIn version 3.1
;   NUMBER OF SEQ ID NOS: 15
; SEQ ID NO 5
;   LENGTH: 684
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: mutant green fluorescent protein
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(684)
;   OTHER INFORMATION:
US-11-021-014-5

```
Query Match          58.8%;   Score 626.4;  DB 10;  Length 684;
Best Local Similarity 94.7%;  Pred. No. 5.1e-178;
Matches 648;  Conservative 0;  Mismatches 36;  Indels 0;  Gaps 0;

Qy    102 AAGGGTGTGATTAAACCAGACATGAAGATGAAGCTGCGTATGGAAGGTGCTGTAAACGGGG 161
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGAGTGTGATAAAACCAGACATGAAGATCAAGCTGCGTATGGAAGGTGCTGTAAACGGGG 60

Qy    162 CACAAGTTCGTGGTTGAAGGAAGCGAAAAGGAAGCCTTTCAGACGCGGAACACAGACTATG 221
          |||||||||||||||||  ||||||||||||||||||||  |||||||||||||||||||
Db     61 CACAAGTTCGTGATTGAAGGAAGCGAAAAGGAAGCCTTTCGAGGGAAAAACAGACTATG 120

Qy    222 GACCTTACAGTCATAGAGAGGCGCACCATTGCCTTTCGCTTACGATATCTTGACAACAGTA 281
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GACCTTACAGTCATAGAGAGGCGCACCTTGCCTTTCGCTTACGATATCTTGACAACAGTA 180

Qy    282 TTCGATTACGGCAACACAGGGTATTCGGCCAAATACCCAGAAGACATAGCAGATTATTCAAG 341
          |||||||||||||||||||||||||||||||||||| |||| |||||||||||||||||
Db    181 TTCGATTACGGCAACACAGGGTATTCGCCAAATACCCAAAAGACTATTTCAAG 240

Qy    342 CAGACGTTTCCTGAGGGTACTTCTTGGGAACGAAGCATGACATACAGAAGACCAGGGCATT 401
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CAGACGTTTCCGGAGGGTACTCCTGGGAACGAAGCATGACATACAGAAGACCAGGGCATT 300

Qy    402 TGCATCGCCACAAACGACATAACAGCTGATGAAGGCGTCGACGACTGTTTTGCCTATAAA 461
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TGCATCGCCACAAACGACATAACAGCTGATGAAGGCGTCGACGACTGTTTTGTCTATAAA 360

Qy    462 ATTCGATTTGATGGTGTGAACTTTCCTGCCAATGTCCAGTTATGCAGAGGAAAGACGCTG 521
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ATTCGATTTGATGGTGTGAACTTTCCTGCCAATGTCCAGTTATGCAGAGGAAAGACGCTA 420

Qy    522 AAATGGGAGGCCATCCACTGAGATAATGTATGCGCGTGATGGAGTGCTGAAGGGTGATGTT 581
          ||||||||||||||||||||  ||||||||||||||||||||||||||||||||||
Db    421 AAATGGGAGGCCATCCACTGAAAAATGTATGCGCGTGATGGGGTACTGAAGGGTGATGTT 480

Qy    582 AACATGGCTCTGTTGCTTGAAGGAGTGGCCATTACGATCGTGACTTCAAAACTACTTAC 641
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 AACATGGCTCTGTTGCTTGAAGGAGTGGCCATTACGATCGTGACTCCAAAACTACTTAC 540

Qy    642 AAAGCTAAGAAGGTTGTCCGGTTCCAGACTATCACTTTGTGGACCATCGCATTGAGATT 701
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 AAAGCTAAGAAGGTTGTCCAGTTGCCAGACATCATTTTGTTGACCATCGCCATTGAGATT 600

Qy    702 GTGAGCCACCACAAAGATTACCACAAGGTTAAGCTACGACGACCGAGCTCGTCAT 761
          |||||||||||||||||||||||||||||||||||| |
Db    601 GTGAGCCACGACAAAGATTACAACAAGGTTAAGCTGTATGAGCATGCCGAAGCTTCATTCT 660

Qy    762 GGACTGTCAAGGAAGGCCAAGTAA 785
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; SEQ ID NO 15

RESULT 9
US-10-757-356-15
; Sequence 15, Application US/1075356
; Publication No. US2005003208541
; GENERAL INFORMATION:
;   APPLICANT: Labas, Yulii Aleksandrovich
;   APPLICANT: Gurskaya, Nadezda Georgievna
;   APPLICANT: Yanushevich, Yuriy
;   APPLICANT: Fradkov, Arcady Fedorovich
;   APPLICANT: Lukyanov, Konstantin
;   APPLICANT: Lukyanov, Sergey
;   APPLICANT: Matz, Mikhail Vladimirovich
;   TITLE OF INVENTION: NOVEL CHROMOPHORES/FLUOROPHORES AND
;   TITLE OF INVENTION: METHODS FOR USING THE SAME
;   FILE REFERENCE: CLON-090
;   CURRENT APPLICATION NUMBER: US/10/757,356
;   CURRENT FILING DATE: 2004-01-13
;   PRIOR APPLICATION NUMBER: 60/332,980
;   PRIOR FILING DATE: 2001-11-13
;   PRIOR APPLICATION NUMBER: PCT/US02/36499
;   PRIOR FILING DATE: 2002-11-12
;   NUMBER OF SEQ ID NOS: 28
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
;   LENGTH: 795
;   TYPE: DNA
;   ORGANISM: Montastraea cavernosa
US-10-757-356-15

```
Query Match          50.0%;   Score 533.4;  DB 8;  Length 795;
Best Local Similarity 83.2%;  Pred. No. 6.9e-150;
Matches 680;  Conservative 0;  Mismatches 101;  Indels 36;  Gaps 5;

Qy      1 ATTCGCCCTGGTGATTTGGAAGAGCAGCAGATCGAGAACAACAAGAGCTG--TAAGGTTGA 58
          |||  |||  |||||||||||||||||||||||||||  |||||||||||||
Db      9 ATTCACCCTGGTGATTTGGAAGAGAGCAGCAGACCGAGAACAACAAGAGCTGTGTATAAGGCTGA 68

Qy     59 TATCTTAC-TTACGTCTACCATCATGACAAGTGTTGCACAGAAAAGGGTGATTAAAC 117
          ||||||| |||||||||||||||||||||||
Db     69 TATCTTACTTTACGTCTACCATCATGA------------GTGTGATTAAAT 107

Qy    118 CAGACATGAAGATGAAGCTGCGTATGGAAGGTGCTGTAAACGGGACCAAGTTCGTGGTTG 177
          ||||||||||||||||||||||||||||||||  ||||||||||||||||||||||
Db    108 CAGTCATGAAGATCAAGCTGCGTATGGAAGGTGAAAGGCAGTGTAAACGGGCACAACTTCGTAATTG 167

Qy    178 AAGGAGATGAAAAGGGAAGCCTTTCGACGGACACAGACATTATTCAAGGGATCCTTACCAGTCATAG 237
          |||||||||||||||||||  |||||  ||||||||||||||||
Db    168 TTGGAGAAGGAAGGCAAGCCTTTATGAGGGAACACAGAGTGACCAGTCACAGTCAAAG 227

Qy    238 AAGGGCGCACCATTGCCTTTCGCTTACGATATCTTGACAACAGTATTCGGCAACA 297
          |||||||||||||||||||||  |||||||  |||||||||||||
Db    228 AAGGGCGCACCTCTGCCTTTGCCTTCGATATCATGACAACAACAGTATTCGGCAATA 287

Qy    298 GGGTATTCGCCAAATACCCAGAAGACATAGCAGATTATTTCAAGCAGACGCTTCCTGAGG 357
          |||||||||  |||||||||||  | |||  |||||||||||||  ||||||||||||||
Db    288 GGGTATTCGCAAAATACCCAAAAACATATCCCAGACTCATTTCAAGCAGCAGATGTTTCCTGAGG 347

Qy    358 GGTACTTCTGGGAACGAAGCATGACATACGACAAGAACCAGGGCGGGGGCATCCATCACG 417
          ||||||||||||||||||||||||||||||||  ||||||||||||
Db    348 AGTATTCCTGGGAACGAAGCAAGCATGAATTTCGAAGGCGGGGCATTTGCACCGCCAGGAACG 407

Qy    418 ACATAACAATGATGATGAAGGAAGGCGTCGCGACTGTTTTGCCTATAAAATTCGATTTGATGGTG 477
          ||||||||||  |||||||||||||||||  |||||||||||||
Db    408 AGATAACAATG------GAAGGCGACTGTGTTTTTCAATAAAGTTCGATTTGATTGGTG 458

Qy    478 TGAACTTTCCTGCCAATGTCCAGTTATGCAGAGGAAGAAGACCTGAAATGGGAGGCCATCCA 537
          |||||||||||||||||||||||||||||||||||||||||||||
Db    459 TGAACTTCCCCCCAATGGTCCAGTCATGCAGCAGAAGAAGAGACGCTGAAATGGGAGGCCATCCA 518
```

Qy   538 CTGAGAGATAATGTATGCGCGTGATGGAGTGCTGAAGGGTGATGTTAACATGGCTCTGTTGC 597
          ||||| |||| |||| |||||||||||||||| || ||||| ||| ||||||| |||||||
Db   519 CTGAAAAAATGTATGCGCGTGATGGAGTGCTGACGGGTGATATCCAACATGGCTTTGTTGC 578

Qy   598 TTGAAGGAGGTGGCCATTACCGATGTGACTTCAAAACTACTTACAAAGCT---AAGAAGG 654
          |||||||||||||||||||||||||||||||||||| || ||||||||||| |||||||
Db   579 TTGAAGGAGGTGGCCATTACCGATGTGACTTCAGAACTACTTACAGAGCTTAAGAAGAAGG 638

Qy   655 TTGTCCGGTTGCCAGACTATCACTTGTGCACCATGCGCATTGAGATTGTGAGCCACGACA 714
          ||||| |||| | ||||| || ||| | | ||| |||| || |||||||||||||||||
Db   639 GTGTCAAGTTACCAGATTATCACTTTGAGATCACTCCATTGAGATTTGCGCCATGACA 698

Qy   715 AAGATTACAACAAGGTTAAGCTGCACGAGCGATGCGAAGCTCGTCATGGACTGTCAAGGA 774
          |||| |||| ||||||||||| || |||| || || |||||||| | ||| |||||||||
Db   699 AAGATACACTGACGTTAAGCTTAACGAGCATGCGAAGCTCATTCTGGGCTGCTGCCGAGG 758

Qy   775 AGGCCAAGTAAAGGCTTAATGAAAAGTCAAGACGACA 811
          ||||||||||||||||||||| ||||||||||||||
Db   759 TGGCCAAGTAAAGGCTTAACGAAACGCCAAGACCACA 795

RESULT 10
US-10-244-779-1
; Sequence 1, Application US/10244779
; Publication No. US20030106078A1
; GENERAL INFORMATION:
; APPLICANT: Falkowski, Paul
; APPLICANT: Sun, Yi
; APPLICANT: Gorbunov, Maxim
; APPLICANT: Wyman, Kevin
; APPLICANT: Chen, Yi-Bu
; TITLE OF INVENTION: mcFP Encoding Nucleic Acids,
; TITLE OF INVENTION: Polypeptides, Antibodies and Methods of Use Thereof
; FILE REFERENCE: Rut 00-0023US
; CURRENT APPLICATION NUMBER: US/10/244,779
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: 60/322,189
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FascSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 860
; TYPE: DNA
; ORGANISM: Montastrea cavernosa
US-10-244-779-1

Query Match   48.5%; Score 517.2; DB 5; Length 860;
Best Local Similarity   80.5%;   Pred. No. 5.7e-145;
Matches 668; Conservative   0; Mismatches 128; Indels   34; Gaps   4;

Qy   1 ATTTCGCCCTGGTGATTTGGAAGAGAAGCAGCAGCAGCAGAACAACAGAGCTGTAAGGTTGATA   60
          ||||||||||||||||||||| ||||||||||||||| |||| |||||||| |||||||||||
Db   54 ATTCACCCTGGTGATTTGGAAGCGGAGCCGAGCAAATCTAGAAGAACAACAGCGCTGTAAGACTGATA 113

Qy   61 TCTTAC-TTACGTCTACCATCATGACAAGTGTTCCACAGGAAAAGGGTGTGATTAAACCA 119
          |||||| |||||||||||||||||| ||||| ||
Db   114 TCTTACTTTACGTCTACCATCATGA-------------------GTGTGATTAAATCA 152

Qy   120 GACATGAAGATGAAGCTGCGTATGGAAGGTGCTGTGAAACGGGCACAAGTTCGTGGTTGAA 179
          |||||||| || ||||||||||||||||||||||||||||||| |||||||||||||||||
Db   153 GTCATGAAAATCAAGCTGCGTATGGACGGGCATGGGCACAGTTAAACGGGCACAAGTTCATGATTACA 212

Qy   180 GGAGATGAAGAAAGGGAAGCCTTTCGACGAGAACAGAGAACTCATATGATGAGTCAGTCAGTCATAGAA 239
          ||||||||||||||||||| || | ||||| |||||| ||| |||||||| |||||||| ||||||
Db   213 GGAGAAGGTGAAGGCAAGCCTTTCGAGGGGCCGCTGTGAACGGGCCTGTGAACGGGG 272

Qy   240 GGGCCACCATTGCCTTTCGCTTACGATATCTTGACAACAGTATTCGGCAACAGG 299
          |||||||| ||| |||||||||||| |||| || ||||| |||| |||| ||||
Db   273 GGGCGAACCTGCCTTTCGCCTTACGACATCTTGACAACAGCATTTCAGTACGGCAACAGG 332

Qy   300 GTATTCGCCAAATACCCAGAAGACATAGCAGATTATTTCAAGCAGACGTTTCCTGAGGGG 359
          |||||| ||||||||||| ||| |||| |||| ||| ||||| |||||| || |||||||
Db   333 GTATTCACCAAAGACATACCCAAAGACATAGCAGATATTTCAAGCAGTCAGTAATTTCAGCAGCAGCAGCG 392

Qy   360 TACTTCTGGGAACAAGCAGCATGAAGCATACGAAGACCAGGGCGATTTGCATCGCCACAAAACGAC 419
          ||||||||||||| || ||||| || ||||||||||| || ||||||||| || ||||||||| ||
Db   393 TATTCCTGGGAAAGAAGAGAGCATGAAGCATACAGGGCGTTTGCATCGTCACACGAC 452

Qy   420 ATAACAATGATGGAAGCGTCGACGACTTTCGATTGTGATTTGATGTGTGTG 479
          ||||||||||||||||| ||| | | |||||||||||||||||||||||
Db   453 ATAAAGTTG---------GAAGGCGACTGTTTTTCTACGAAATTCGATTTTATGTGTGTG 503

Qy   480 AACTTCCTGCCAATGTCCAGTTATGCAGAGGAAGACGCTGAAATGGGAGCCATCCACT 539
          |||||||| |||||||||||||||| |||||||| |||||||||||||||||||||||
Db   504 AACTTTCCCTCCCAGTGGTCCAGTTATGCAGAATGCGCTGAAATGGGAGCCATCCACT 563

Qy   540 GAGATAATGTATGCGCGTGATGAGTGCTGAAGGGTGATGTTAACATGGCTCTGTTGCTT 599
          |||| ||||||||||||||||||| |||| |||| |||||||||||||| ||| || |||
Db   564 GAGAATATGTACGTGCGTGATGGAGGATGCTACTGTGGGGGATGGTTAGCAGGACCCTGTTGCTT 623

Qy   600 GAAGGAGGTGGCCATTACCGATGTGACTTGATGTGAGCCACGACACAAAGAT 659
          ||||||||||||||||||||||||||||| || |||||||||||||||||||
Db   624 GAAGGGGGATAAAACATCACCGATGTAACTTCAGAGTACTTACGGCGCAAAAAGGAGGTGTC 683

Qy   660 CGGTTGCCAGACTATCACTTGTGCACCATGCCATTGAGATTGTGAGCCACGACAAAGAT 719
          |||||||||| |||||||||||| |||||||||| |||||||||||||||||| ||||||
Db   684 GTGTTGCCAGAATATCACTTGTTGGACCACGAATTGAATTCTGAGCCATGACAACAAAGAT 743

Qy   720 TACAACAAGGTTAAGCTGCACGAGCGATGCCGAGCTCG---TCATGGACTGTCAAGGAAG 776
          |||| |||||||||| || | | |||| || |||| | |||| || ||| ||||||
Db   744 TACACACCGTTGAGGTGTATGAGAATGCGTTGCTGCCCTTCTCATGCTGTCGCCGGTTAAG 803

Qy   777 GCCAAGTAAAGGCTTAATGAAAAGTCAAGACGAGAAACAA 826
          |||||||||||||||| |||||||||| ||||||||| ||
Db   804 GCCAAGTAAAGGCTTAACTAACATAAAGGCCCAAACGACCAAGAGGAGAAAAAA 853

RESULT 11
US-10-851-636-12
; Sequence 12, Application US/10851636
; Publication No. US20050048609A1
; GENERAL INFORMATION:
; APPLICANT: Matz, Mikhail
; APPLICANT: Kelmanson, Ilya
; APPLICANT: Salih, Anya
; APPLICANT: Meleshkevitch, Ella
; TITLE OF INVENTION: Novel Fluorescent and Colored Proteins, and Polynucleotides that
; TITLE OF INVENTION: Encode These Proteins
; FILE REFERENCE: UF-364XC1
; CURRENT APPLICATION NUMBER: US/10/851,636
; CURRENT FILING DATE: 2004-05-20
; PRIOR APPLICATION NUMBER: 60/472,196
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 729
; TYPE: DNA
; ORGANISM: Montastraea cavernosa
US-10-851-636-12

Query Match   47.6%; Score 507.4; DB 9; Length 729;
Best Local Similarity   85.8%;   Pred. No. 4.7e-142;
Matches 591; Conservative   0; Mismatches 86; Indels   12; Gaps   2;

Qy   102 AAGGGTGTGATTAAACCAGAACATGAAGATGAAGCTGCGTATGGAAGGTGCTGTAAACGGG 161
          ||||||||||| || ||||||||||| || |||||||||||||||||||||||| |||||||
Db   25 ATGAGTGTGATTAAACCAGAACATGAAGATGAAGCTGCGTATGGAAGGGCGTGTAAACGGG 84

Qy   162 CACAAGTTCGTGGTTGAAGGAGATGAAGAAAGGGAAGCCTTTGACGAACACGACTATG 221
          |||||||||||| ||||||| || |||||||||||||||||||||| | |||||||||
Db   85 CACAACTTCGTGATTGAAGGAGGAGAAGGCAAGCCTTTCGAGGGGACCACGACTATA 144

Qy   222 GACCTTACAGTCATAGAAGGCGCACCATTGCCTTTCGCTTACGATATCTTGACAACAGTA 281
          || ||||| |||| ||||||||||||| ||||||||| || || ||||| ||||| || |
Db   145 AACCTTACAGTCAAAGAAGGCGGCACCATCCTGCCTTTTGCTTACGATATCTTGACGATCAGCA 204

Qy 222 GACCTTACAGTCATAGAAGGGCGCACCATTGCCTTCGCTTACGATATCTTGACAACAGTA 281
        |||||||||||| ||||| ||| ||| ||||||| ||||||||||||||||||||| |||
Db 121 AACCTTACAGTCAAGAAGAGGCGGACCGACCTCGCCCTTTGCTTACGATATCTTGACAGCAGCA 180

Qy 282 TTCGATTACGGCAACACAGGGTATTCGCCAAATACCCAGAAGACATAGCAGATTATTCAAG 341
        ||| ||||||||||||| |||||||| ||||||||||||||||||||||||| ||||||||
Db 181 TTCCAGTACGGCAACAGGGCATTCACCAAATACCCAGAAGACATAGCAGACTATTCAAG 240

Qy 342 CAGACGTTCCTGAGGGTACTTCTGGAACGGTCGCGACTGTTTGCCTATAAA 401
        |||| ||||||||||| |||||| |||| | | ||||| ||| |||||
Db 241 CAGTCTTTTCCTGAGGGTATTCGGACACTAAGAGCGACTGCTTTATCTATGAA 300

Qy 402 ATTCGATTGATGGTGTGAACTTCCTGCCAATGGTCCAGTTATGCAGAGGAAGACGCTG 461
        ||| ||||||||| ||||| |||| |||||||||||||| |||| ||| | ||||||||
Db 301 TGCATCATCAAGAGCGGACATAAGAATG--------GAAGGCGGACTGCTTTATCTATGAA 351

Qy 462 AAATGGGAGCCATCCACTGAGATAATGTATGCGCGTGATGAGGGTGAAGGGTGATGTT 521
        ||||||||||||||||||||| ||||||||| ||| ||||| |||||||||||||||||
Db 352 ATTCGATTGATGGTGTGAACTTCCTGCCAATGGTCCAGTTATGCAAAGAGACGCTG 411

Qy 522 AAATGGGAGCCATCCACTGAGATAATGTATGCGCGTGATGAGGGTGAAGGGTGATGTT 581
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 412 AAATGGGAGCCATCCACTGAGATAATGTATGCGTGATGAGGGTGATGAGGGTGATGTT 471

Qy 582 AACATGGCTCTGTTGCTTGAAGGAGGTGGCCATTACCGATGTGACTTCAAAACTACTTAC 641
        ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db 472 AACATGGCTCTGTTGCTTGAAGGAGGTGGCCATTACCGATGTGAAGTGACTACTTAC 531

Qy 642 AAAGCTAAGAGGTTGTCCGGTTGCACGAGCCGAGAATGCCGAGCTCG---T 701
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Db 532 AAAGCGAAGAAACGTGTTCAGTTGCCAGACTATCACTTTGTGGACACCGCATTGAGATT 591

Qy 702 GTGAGCCACGACGACAAAGATTACACAACAAGGTTAAGCTGCACGATGCCGAAGCTCGTCAT 761
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Db 592 TTGAGCCATGCCATGCTTCAGTTGCCAGACTATCACTTTGTGGACACCGTAAGCGTCGCTAT 651

RESULT 13
US-10-851-636-13
; Sequence 13, Application US/10851636
; Publication No. US20050048609A1
; GENERAL INFORMATION:
; APPLICANT: Matz, Mikhail
; APPLICANT: Kelmanson, Ilya
; APPLICANT: Salih, Anya
; APPLICANT: Meleshkevitch, Ella
; TITLE OF INVENTION: Novel Fluorescent and Colored Proteins, and Polynucleotides that
; TITLE OF INVENTION: Encode These Proteins
; FILE REFERENCE: UF-364XC1
; CURRENT APPLICATION NUMBER: US/10/851,636
; CURRENT FILING DATE: 2004-05-20
; PRIOR APPLICATION NUMBER: 60/472,196
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 729
; TYPE: DNA
; ORGANISM: Montastraea cavernosa
US-10-851-636-13

Query Match 46.7%;   Score 497.8; DB 9; Length 729;
Best Local Similarity 84.9%; Pred. No. 3.8e-139;
Matches 585; Conservative 0; Mismatches 92; Indels 12; Gaps 2;

Qy 102 AAGGGTGATTAAACCAGACATGAAGATGAAGCTGCGTATGGAAGGTGCTGTAAACGGG 161
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Db 25 ATGAGTGTGATTAAACCAGAATGAAACCAGAATGAAGATCAAGCTGCGTATGCTGCGTTGAAACGGG 84

Qy 162 CACAAGTTCGTCGTTGAAGGAGATGAAGAAAAGGGAAGCCTTTCGACGGAACACAGACTATG 221
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Db 85 CACAACTTCGTGATTGAAGGAGAAGAGAAGGAAAAGGGAAGCCTTTCGAGGGAACACAGACTATA 144

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Qy 282 TTCGATTACGGCAACACAGGGTATTCGCCAAATACCCAGAAGACATAGCAGATTATTCAAG 341
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Db 205 TTCCAGTACGGCAACAGGGCATTCACCAAATACCCAGAAGACATAGCAGACTATTCAAG 264

Qy 342 CAGACGTTCCTGAGGGTACTTCTGGAACGGTCGCGACTGTTTGCCTATAAA 401
        |||| ||||||||||| |||||| |||| | | ||||| || | |||||
Db 265 CAGTCTTTTCCTGAGGGTATTCGGACACTAAGAGCGACTGCTTTATCTATGAA 375

Qy 402 ATTCGATTGATGGTGTGAACTTCCTGCCAATGGTCCAGTTATGCAGAGGAAGACGCTG 461
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Db 376 ATTCGATTGATGGTGTGAACTTCCTGCCAATGGTCCAGTTATGCAAAGAGACGCTG 435

Qy 462 AAATGGGAGCCATCCACTGAGATAATGTATGCGCGTGATGAGGGTGAAGGGTGATGTT 521
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Db 436 AAATGGGAGCCATCCACTGAGATAATGTATGCGTGATGAGGGTGATGAGGGTGATGTT 495

Qy 522 AACATGGCTCTGTTGCTTGAAGGAGGTGGCCATTACCGATGTGACTTCAAAACTACTTAC 581
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Db 496 AACATGGCTCTGTTGCTTGAAGGAGGTGGCCATTACCGATGTGAAGTGACTACTTAC 555

Qy 582 AAAGCTAAGAGGTTGTCCGGTTGCACGAGCCGAGAATGCCGAGCTCG---T 641
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Db 556 AAAGCGAAGAAACGTGTTCAGTTGCCAGACTATCACTTTGTGGACACCGCATTGAGATT 615

Qy 642 GTGAGCCACGACGACAAAGATTACACAACAAGGTTAAGCTGCACGATGCCGAGAGCTCG---T 701
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Db 616 TTGAGCCATGCCATGCTTCAGTTGCCAGACTATCACTTTGTGGACACCGTAAGCGTCTCGCTAT 675

Qy 759 CATGGACTGTCAAGGAGGCCAAGTAAAG 787
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Db 676 TCTATGCTGCCGAGTCAGGCTCAGGCCAAGGAAAG 704

RESULT 12
US-10-851-636-4
; Sequence 4, Application US/10851636
; Publication No. US20050048609A1
; GENERAL INFORMATION:
; APPLICANT: Matz, Mikhail
; APPLICANT: Kelmanson, Ilya
; APPLICANT: Salih, Anya
; APPLICANT: Meleshkevitch, Ella
; TITLE OF INVENTION: Novel Fluorescent and Colored Proteins, and Polynucleotides that
; TITLE OF INVENTION: Encode These Proteins
; FILE REFERENCE: UF-364XC1
; CURRENT APPLICATION NUMBER: US/10/851,636
; CURRENT FILING DATE: 2004-05-20
; PRIOR APPLICATION NUMBER: 60/472,196
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 678
; TYPE: DNA
; ORGANISM: Montastraea cavernosa
US-10-851-636-4

Query Match 47.6%;   Score 507.2; DB 9; Length 678;
Best Local Similarity 86.8%; Pred. No. 5.2e-142;
Matches 573; Conservative 0; Mismatches 78; Indels 9; Gaps 1;

Qy 102 AAGGGTGATTAAACCAGACATGAAGATGAAGCTGCGTATGGAAGGTGCTGTAAACGGG 161
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Qy 162 CACAAGTTCGTCGTTGAAGGAGATGAAGAAAAGGGAAGCCTTTCGACGGAACACAGACTATG 221
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Db 61 CACAACTTCGTGATTGAAGGAGAAGAGAAGGAAAAGGGAAGCCTTTCGAGGGAACACAGACTATA 120

Qy 222 GACCTTACAGTCATAGAGAGGCGCCACCATTGCCTTTCGCTTACGATATCTTGACAACAGTA 281
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Db 145 AACCTTACAGTCAAAGAAGAGGGCGCACCTCCCCTTTGCTTACGACATCTTGACATCAGCA 204

Qy 282 TTCGATTACGGCAACAGGGTATTCGCCAAATACCAGAAGACATAGCAGATTATTTCAAG 341
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Db 205 TTCCAGTATGGCAACAGGGTATTCACCAAATATCCAGACGATATACCAGACCAGAGTATT 264

Qy 342 CAGACGTTTCCTGAGGGGTACTTCTGGGAACGAAGCATGACATACGAAGACACAGGGCATT 401
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Qy 402 TGCATCGCCACAAAGCACATACAATGATGGAAGGCGTCGACGACTGTTTTGCCTATAAA 461
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Db 325 --------GAAGGCGACTGTGTTTATCTTACGAA 375

Qy 462 ATTCGATTTGATGGTGTGAACTTTCCTGCCAATGGTCCAGTTATGCAGAGGAAGACGCTG 521
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Db 376 ATTCAATTTCATGGTGTGAACTTTCCACCCAATGGTCCAGTTATGCAGAGAAGACGCTG 435

Qy 522 AAATGGGAGCCATCCACTGAGATAATGTATGCGCGTGAGGGTGCTGAAGGGTGATGTT 581
        ||||||||| ||||||| |||||| ||||| |||| |||| ||||||| |||||| |||
Db 436 AAATGGGAACCATCCACTGAGATAATGTATGTGCGTGAGGGTGCTGAAGGGTGATGTT 495

Qy 582 AACATGGCTCTGTTGCTTGAAGGAGGTGGCCATTACCCGATGGTGACTTCAAAACTACTTAC 641
        ||||||||| ||||||||||||||||||| |||||| ||||||||| |||| ||||||||||
Db 496 AACATGGCTCTGTTGCTTGAAGGAGGTGGCCATTACCCGATGGTGACTTCAGAAGTACTTAC 555

Qy 642 AAAGCTAAGAAGGTTGTCCGGTTGCACGACTATCACTTTGTGGACCATGCCATTGAGATT 701
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Db 556 AAAGCGAAGAAGATGTTCATTTGCCAGACTATCACTACGTGGACCACCCGCATTGAGATT 615

Qy 702 GTGAGCCACGACAAAGATTACAACAAGGTTAAGCTGCACAGAGCTCGACGAGCTCG---T 758
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Db 616 TTGAGCCATGACATGACAAAGATTACAAAAAATGTTACGCTGTATGAGCATGCCAAGCTCGCTAT 675

Qy 759 CATGGACTGTCAAGGAAGGCCAAGTAAAG 787
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Db 676 TCTATGCTGCCGAGTAAGGCCAAGGAAAG 704

Query Match   46.7%; Score 497.4; DB 9; Length 678;
Best Local Similarity   85.0%; Pred. No. 4.8e-139;
Matches 584; Conservative 0; Mismatches 91; Indels 12; Gaps 2;

Qy 102 AAGGGTGTGATTAAACCAGACATGAGATGAAGATGAAGTCGCTATGGAAGGTGCTGTAAACGGG 161
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Db   1 ATGAGTGTGATTAAACCAGATATATGAAGATCAAGCTGCCGTGCCATGCGCGTTGTAAACGGG 60

Qy 162 CACAAGTTCGTGTTGAAGGAGGATGGAAAAGGAAGGAAGCCTTTCGACGGAACACAGACTATG 221
        ||||||||||||||||| |||| || || || |||||| |||||||| ||| |||||||
Db   61 CACAAGTTCGTGTTGATTAAGGAGAGGAGAGGAGGGCAAGCCTTTCGAGGAACGCAGACTATA 120

Qy 222 GACCTTACAGTCATAGAGAGGCGCCACCATGCCTTTCGCTTACGATATCTTGACAACAGTA 281
        ||||||||||||| ||| ||| ||| || ||||||| |||||| |||||||| |||||
Db 121 AACCTTACAGTCAAAGAAGAGGGCGCACCTCCCCTTTGCTTACGACATCTTGACATCAGCA 180

Qy 282 TTCGATTACGGCAACAGGGTATTCGCCAAATACCAGAAGACATAGCAGATTATTTCAAG 341
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Db 181 TTCCAGTATGGCAACAGGGTATTCACCAAATATCCAGACGATATACCAGACTATTTCAAG 240

Qy 342 CAGACGTTTCCTGAGGGGTACTTCTGGGAACGAAGCATGACATACGAAGACCAGGGCATT 401
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Db 241 CAGACGTTTCCTGAAGGGTATTCGTTATGAAGACCAGAGTATT 300

Qy 402 TGCATCGCCACAAAGCACATACAATGATGGAAGGCGTCGACGACTGTTTTGCCTATAAA 461
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Db 301 TGCACGGCCACAAGCGACCATAAAAATG-------GAAGGCGACTGTTTTATCTCACGAA 351

Qy 462 ATTCGATTTGATGGTGTGAACTTTCCTGCCAATGGTCCAGTTATGCAGAGGAAGACGCTG 521
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Db 352 ATTCAATTTCATGGTGTGAACTTTCCACCCAATGGTCCAGTTATGCAGAGAAGACGCTG 411

Qy 522 AAATGGGAGCCATCCACTGAGATAATGTATGCGCGTGAGGGTGCTGAAGGGTGATGTT 581
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Db 412 AAATGGGAACCATCCACCGAGAAAAATGTATGTGCGTGATGGTGATGAGTGATGTT 471

Qy 582 AACATGGCTCTGTTGCTTGAAGGAGGTGGCCATTACCCGATGGTGACTTCAAAACTACTTAC 641
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Db 532 AAAGCGAAGAAGATGTTCATTTGCCAGACTATCATCACTACGTGGACCACCCGCATTGAGATT 591

Qy 702 GTGAGCCACGACAAAGATTACAACAAGGTTAAGCTGCACAGAGCTCGACGAGCTCG---T 758
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Db 592 TTGAGCCATGCTGACAAAGATTTACAAAAATGTTACGCTGTATGAGCATGCCAAAGCTCGCTAT 651

Qy 759 CATGGACTGTCAAGGAAGGCCAAGTAA 785
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Query Match   45.6%; Score 486.4; DB 9; Length 678;
Best Local Similarity   84.8%; Pred. No. 1e-135;
Matches 560; Conservative 0; Mismatches 91; Indels 9; Gaps 1;

Qy 102 AAGGGTGTGATTAAACCAGACATGAGATGAAGATGAAGTCGCTATGGAAGGTGCTGTAAACGGG 161

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Db    61 CATAATTTCGTGATTGAAGGAGAAGGAAAAAGGAAAATCCTTACGAGGGAACGCAGATTTTA 120

Qy   222 GACCTTACAGTCATAGAGAGGCGCACCATTGCCTTCGCTTACGATATCTTGACAACAGTA 281
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Qy   282 TTCGATTACGGCAACAGGGGTATTCGCCAAATACCCAGAGACACATAGACAGATTATTTCAAG 341
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Qy   342 CAGACGTTTCCTGAGGGGTACTTCTGGGAACGAAGCATGACATACGAAGACCAGGGCATT 401
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Db   241 CAGACTTTTCCTGAGGGGTATCACTGGGAAAGAAGCATGACTTATGAGACCAGGGGCATT 300

Qy   402 TGCATCGCCACAAACGACATAACAATGATGGAAGGCGTCGACGACTGTTTGCCTATAAA 461
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Qy   462 ATTCGATTTGATGGTGTGAACTTTCCTGCCAATGGTCCAGTTCAGAGGAAGACGCTG 521
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Qy   522 AAATGGGAGCCATCCACTGAGATAATGTATGCGCGTGATGGAGTGCTGAAGGGTGATGTT 581
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Db   412 AAATGGGAGCCATCCCACTGAGAAAATGTACGTACGTGATGGAGTGCTCGAAGGGTGATGTT 471

Qy   582 AACATGGCTCTGTTGCTTGAAGGAGGTGGCCATTACCGATGTGACTTCAAAACTACTTAC 641
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Db   472 AACATGGCTCTGTTGCTTGAAGGAGGTGGCCATTATCGATGTGATTTCAAAAACTACTTAC 531

Qy   642 AAAGCTAAGAAGGTTGTCCGGTTGCCAGACTATCACTTTGTGGACCATCGCATTGAGATT 701
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Db   532 AAAGCAAAGAAGGATGTCCGTTTGCCAGACTATCACTTTGTGGACCACCGCATTGAGATT 591

Qy   702 GTGAGCCACGACAAAGATTACACACAAGGTTAAGCTGCACGAGCATGCCGAAGCTCGTCAT 761
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Db   592 TTGAAGCATGACAAAGATTACACAACAAGGTCAAGCTCTATGAGAAATGCCGTTGCTCGCTAT 651
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OM nucleic - nucleic search, using sw model

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GenCore version 5.1.7

Run on: April 5, 2006, 21:14:53 ; Search time 666 Seconds
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Score	Query Match	Length	DB	ID	Description
1	256.6	24.1	678	8	US-10-209-208-2	Sequence 2, Appli
2	256.6	24.1	678	14	US-11-218-880-2	Sequence 1, Appli
3	256.6	24.1	678	14	US-11-100-988-1	Sequence 1, Appli
4	252	23.6	876	14	US-11-082-154A-39	Sequence 39, Appli
5	230	21.6	678	14	US-11-100-988-4	Sequence 4, Appli
6	226	21.2	645	11	US-11-208-927-1	Sequence 1, Appli
7	223.6	21.0	678	8	US-10-209-208-5	Sequence 5, Appli
8	223.6	21.0	678	14	US-11-218-880-5	Sequence 5, Appli
9	219.8	20.6	678	11	US-11-187-622-7	Sequence 7, Appli
10	219.8	20.6	681	8	US-10-209-208-3	Sequence 3, Appli
11	219.8	20.6	681	8	US-10-209-208-23	Sequence 23, Appli
12	219.8	20.6	681	14	US-11-218-880-3	Sequence 3, Appli
13	219.8	20.6	681	14	US-11-218-880-23	Sequence 23, Appli
14	219.8	20.6	4692	14	US-11-082-154A-29	Sequence 29, Appli
15	215.8	20.2	675	11	US-11-187-622-13	Sequence 13, Appli
16	215.8	20.2	678	11	US-11-187-622-14	Sequence 14, Appli
17	215.8	20.2	1635	11	US-11-205-740-3	Sequence 3, Appli
18	215.8	20.2	1635	11	US-11-205-740-9	Sequence 9, Appli
19	215.8	20.2	1635	11	US-11-205-740-11	Sequence 11, Appli
20	215.8	20.2	6706	8	US-10-655-872-4	Sequence 4, Appli
21	215.8	20.2	7927	8	US-10-655-872-7	Sequence 7, Appli
22	214.2	20.1	1815	11	US-11-205-740-4	Sequence 4, Appli
23	214.2	20.1	1815	11	US-11-205-740-10	Sequence 10, Appli
24	214.2	20.1	1815	11	US-11-205-740-12	Sequence 12, Appli
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26	214.2	20.1	2361	11	US-11-205-740-7	Sequence 7, Appli
27	214.2	20.1	2625	11	US-11-205-740-2	Sequence 2, Appli
28	214.2	20.1	2625	11	US-11-205-740-8	Sequence 8, Appli
29	212.4	19.9	681	8	US-10-209-208-7	Sequence 7, Appli
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31	207	19.4	678	14	US-11-187-622-11	Sequence 11, Appli
32	203.2	19.1	687	11	US-11-187-622-1	Sequence 1, Appli
33	199.6	18.7	678	8	US-10-209-208-9	Sequence 9, Appli
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35	196.4	18.4	678	8	US-10-209-208-80	Sequence 80, Appli
36	188.4	17.7	690	11	US-11-187-622-19	Sequence 19, Appli
37	177.8	16.7	865	11	US-11-187-622-5	Sequence 5, Appli
38	176.2	16.5	693	11	US-11-187-622-3	Sequence 3, Appli
39	171	16.0	705	11	US-11-187-622-15	Sequence 15, Appli
40	165	15.5	696	11	US-11-187-622-17	Sequence 17, Appli
41	164.8	15.5	705	11	US-11-187-622-17	Sequence 17, Appli
42	159	14.9	654	11	US-11-187-622-23	Sequence 23, Appli
43	157.2	14.7	707	11	US-11-187-622-21	Sequence 21, Appli
44	132.2	12.4	720	11	US-11-149-015-1	Sequence 1, Appli
45	126	11.8	720	11	US-11-149-015-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-10-209-208-2
; Sequence 2, Application US/10209208
; Publication No.US20050244921A1
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger
; APPLICANT: Campbell, Robert
; APPLICANT: Baird, Geoffrey
; TITLE OF INVENTION: FLUORESCENT PROTEIN VARIANTS AND METHODS
; TITLE OF INVENTION: FOR MAKING SAME
; FILE REFERENCE: UC083.1CP2CP2
; CURRENT APPLICATION NUMBER: US/10/209,208
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: 10/121,258
; PRIOR APPLICATION FILING DATE: 2002-04-10
; PRIOR APPLICATION NUMBER: 09/866,538
; PRIOR APPLICATION FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 09/794,308
; PRIOR APPLICATION FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 678
; TYPE: DNA
; ORGANISM: Discosoma sp.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(678)
; OTHER INFORMATION: wild-type DsRed
US-10-209-208-2

Query Match 24.1%; Score 256.6; DB 8; Length 678;
Best Local Similarity 62.8%; Pred. No. 3.4e-61;
Matches 419; Conservative 0; Mismatches 239; Indels 9; Gaps 1;

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Qy  102 AAGGGTGTGATTAAACCAGACATGAAGCTGCGTATGGAAGGTGCTCGTAAACGGG 161
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Qy  162 CACAAGTTCGTCGTTGAGGAGGTTGAAGGAGATGAGAAAAGGAAGAAGCCTTTCGACGGAACACAGACTATG 221
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Query Match   24.1%;   Score 256.6;   DB 14;   Length 678;
Best Local Similarity 62.8%;   Pred. No. 3.4e-61;
Matches 419;   Conservative 0;   Mismatches 239;   Indels 9;   Gaps 1;

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Qy  102 AAGGGTGTGATTAAACCAGACATGAACGATGAGAGCTGCGTATGGAAGGTGCTGTAAACGGG 161
            ||| || ||||| || ||  || ||| | ||| ||  |||| |  ||||||| ||| ||||
Db   13 AAGAATGTTATCAAGGAGTTCATGAGGTTTAAGGTTCGCATGGAAGGACGGTCAATGGG 72

Qy  162 CACAAGTTCGTCGTTGAAGGAGATGAAAAAGGAAGGAAGCCTTCGACGAACACAGACTATG 221
            || |||| |||||  || || || |||| || ||| || ||||  ||| ||  ||| ||
Db   73 CACGAGTTTGAAATAGAAGGGCGAAGGAGAGGGGAGCCACATCAGAAGCCACCATACCGTA 132

Qy  222 GACCTTACAGTCATAGAGAGCGCCACCATTGCCTTTCGCTTACGATATCTTGACAACAGTA 281
            || |||| |||| || ||| || ||||||||| ||| | |||  || || ||| |||||
Db  133 AAGCTTAAGGTAACCAAGGGGGACCTTTGCCATTTGCTTGGGATATTTTGTCACCACAA 192

Qy  282 TTCGATTACGGCAACAGGGTATTCGCCAAATACCCAGAAGACATAGCAGATTATTTCAAG 341
            ||| ||||   ||| ||| || || || || ||||  ||||| || ||  |||| ||
Db  193 TTTCAGTATGGAAGCAAGGTATATGTCAAGCACCCTGCCGACATATAAAAAG 252

Qy  342 CAGACGTTCCTGAGGGGTACTTCTGGAACGAAGCAGATGACATACGAAGACCAGGGCATT 401
            || ||  |||| || ||| ||||  ||| ||| | ||  || || |||| ||  ||
Db  253 CTGTCATTTCCTGAAGGATTTAAATGGAAAGGGTCATGAACTTTGAAGACCGGTGGCGTC 312

Qy  402 TGCATCGCCACAAACGACGACATAACAATGATGGAAGGCCGTCGACGACTGTTTTGCCTATAAA 461
            ||||   |||||  ||| || || || || ||| |  || || |
Db  313 GTTACTGTAACCCAGGATTCCAGTTGCGACGGATGG---------CTGTTTCATCTCACAAG 363

Qy  462 ATTCGATTGATGGTGAACTTTCCTGCCAATGGTCCAGTTATGCAGAGGAAGACGCTG 521
            || |||| || || |||| ||||  || || || || || || ||| || ||| |
Db  364 GTCAAGTTCATTGGCGTGAACTTTCCTTCCGATGGACCTGTTTATGCGGATGCAATG 423

Qy  522 AAATGGGAGCCATCCACTGAGATAATGTATCGCGTGATGAGTGCTGAAGGGTGATGTT 581
            ||| ||||||| |||| |||| ||  || |  ||  || ||| || |||| || |||
Db  424 GGCTGGGAAGCCAGCAGCACTGAGCTTGTATCCTCGTGATCCCGTTGTGTTGAAAGGAGAGATT 483

Qy  582 AACATGGCTCTGTTGCTTGAAGCGTGGCCATTACCGATGTGACTTCAAAACTACTTAC 641
            ||| |||||||| || |||||| ||  |||||| || |  || || ||| || |||
Db  484 CATAAGGCTCTGAAGCTGGTCATTACCTAGTTGAATTCAAAGTATTTAC 543

Qy  642 AAAGCTAAGAGAGGTTGTCCGGTTGCCAGACTATCACTTTGTGGACCATTCGCATTGAGATT 701
            ||| |||||| |||||| ||| ||  ||| || |||  || |  || ||||| |  ||||
Db  544 ATGGCAAAGAAGCCCTGTGCAGCTGACACCTACCAGGGTACTACTATGTGACTCCAAACTGGATATA 603

Qy  702 GTGAGCCACGACAAAGATTACAACACAGGTTAAGCTGCCACGAGCCATGCCGAAGCTCGTCAT 761
            || ||||| ||| ||| |||| || ||  ||| |  |||  || || |||| |||| ||||
Db  604 ACAAGCCACAACGAGCACTATACAATCGTTGAGCAGTATGAAAGAACCGAGGGACGGCCGCCAC 663

Qy  762 GGACTGT 768
            ||| |||
Db  664 CATCTGT 670
```

RESULT 2
US-11-218-880-2
; Sequence 2, Application US/11218880
; Publication No. US2006003420A1
GENERAL INFORMATION:
;   APPLICANT: Tsien, Roger
;   APPLICANT: Campbell, Robert
;   TITLE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT
;   TITLE OF INVENTION: PROTEIN VARIANTS AND METHODS FOR MAKING SAME
;   FILE REFERENCE: UC083.1CP2CP1
;   CURRENT APPLICATION NUMBER: US/11/218,880
;   CURRENT FILING DATE: 2005-09-01
;   PRIOR APPLICATION NUMBER: US/10/121,258
;   PRIOR FILING DATE: 2002-04-10
;   PRIOR APPLICATION NUMBER: 09/794,308
;   PRIOR FILING DATE: 2001-02-26
;   PRIOR APPLICATION NUMBER: 09/866,538
;   PRIOR FILING DATE: 2001-05-24
;   NUMBER OF SEQ ID NOS: 78
;   SOFTWARE: FastSEQ for Windows Version 4.0
;   SEQ ID NO 2
;   LENGTH: 678
;   TYPE: DNA
;   ORGANISM: Discosoma sp.
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(678)
;   OTHER INFORMATION: wild-type DsRed
US-11-218-880-2

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Db   73 CACGAGTTTGAAATAGAAGGGCGAAGGAGAGGGGAGCCACATACCGTA 132
Qy  222 GACCTTACAGTCATAGAGAGCGCCACCATTGCCTTTCGCTTACGATATCTTGACAACAGTA 281
Db  133 AAGCTTAAGGTAACCAAGGGGGACCTTTGCCATTTGCTTGGGATATTTTGTCACCACAA 192
Qy  282 TTCGATTACGGCAACAGGGTATTCGCCAAATACCCAGAAGACATAGCAGATTATTTCAAG 341
Db  193 TTTCAGTATGGAAGCAAGGTATATGTCAAGCACCCTGCCGACATATAAAAAG 252
Qy  342 CAGACGTTCCTGAGGGGTACTTCTGGAACGAAGCAGATGACATACGAAGACCAGGGCATT 401
Db  253 CTGTCATTTCCTGAAGGATTTAAATGGAAAGGGTCATGAACTTTGAAGACCGGTGGCGTC 312
Qy  402 TGCATCGCCACAAACGACGACATAACAATGATGGAAGGCCGTCGACGACTGTTTTGCCTATAAA 461
Db  313 GTTACTGTAACCCAGGATTCCAGTTGCGACGGATGG--------CTGTTTCATCTCACAAG 363
Qy  462 ATTCGATTGATGGTGAACTTTCCTGCCAATGGTCCAGTTATGCAGAGGAAGACGCTG 521
Db  364 GTCAAGTTCATTGGCGTGAACTTTCCTTCCGATGGACCTGTTTATGCGGATGCAATG 423
Qy  522 AAATGGGAGCCATCCACTGAGATAATGTATCGCGTGATGAGTGCTGAAGGGTGATGTT 581
Db  424 GGCTGGGAAGCCAGCAGCACTGAGCTTGTATCCTCGTGATCCCGTTGTGTTGAAAGGAGAGATT 483
Qy  582 AACATGGCTCTGTTGCTTGAAGCGTGGCCATTACCGATGTGACTTCAAAACTACTTAC 641
Db  484 CATAAGGCTCTGAAGCTGGTCATTACCTAGTTGAATTCAAAGTATTTAC 543
Qy  642 AAAGCTAAGAGAGGTTGTCCGGTTGCCAGACTATCACTTTGTGGACCATTCGCATTGAGATT 701
Db  544 ATGGCAAAGAAGCCCTGTGCAGCTGACACCTACCAGGGTACTACTATGTGACTCCAAACTGGATATA 603
Qy  702 GTGAGCCACGACAAAGATTACAACACAGGTTAAGCTGCCACGAGCCATGCCGAAGCTCGTCAT 761
Db  604 ACAAGCCACAACGAGCACTATACAATCGTTGAGCAGTATGAAAGAACCGAGGGACGGCCGCCAC 663
Qy  762 GGACTGT 768
Db  664 CATCTGT 670
```

RESULT 3
US-11-100-988-1
; Sequence 1, Application US/11100988
; Publication No. US20060008878A1
GENERAL INFORMATION:
;   APPLICANT: Glick, Benjamin S.
;   APPLICANT: Bevis, Brooke
;   APPLICANT: Strongin, Daniel E.
;   APPLICANT: Baker, David
;   APPLICANT: Scalley-Kim, Michelle
;   TITLE OF INVENTION: MONOMERIC RED FLUORESCENT PROTEINS
;   FILE REFERENCE: 092234-9002-US01
;   CURRENT APPLICATION NUMBER: US/11/100,988
;   CURRENT FILING DATE: 2005-04-07
;   PRIOR APPLICATION NUMBER: US 60/560,340
;   PRIOR FILING DATE: 2004-04-07
;   NUMBER OF SEQ ID NOS: 5
;   SOFTWARE: Patentin version 3.2
;   SEQ ID NO 1
;   LENGTH: 678

; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: wild-type red fluorescent protein based on Discosoma species
US-11-100-988-1

Query Match   24.1%;   Score 256.6; DB 14;   Length 678;
Best Local Similarity   62.8%;   Pred. No. 3.4e-61;
Matches 419;   Conservative   0;   Mismatches 239;   Indels   9;   Gaps   1;

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Qy  102 AAGGGTGTGATTAAACCAGACATGAAGATGAAGCTGCGTATGGAAGGTGCTGTAAACGGG 161
        |||  ||||  | |||||||||||| ||||| |||||||||||||||||||| |||||||
Db   13 AAGAATGTTATCAAGGAGTTCATGAGGTTTAAGGTTCGCATGGAAGGAACCGTCAATGGG  72

Qy  162 CACAAGTTCGTGGTTGAAGGAGATGAAAAGGGAAGCCTTTCGACCGAACACAGACTATG 221
        ||| ||||  ||  |||||| ||||| ||||||  ||| |  |  || ||  | |  ||
Db   73 CACGAGTTTGAAATAGAAGGCGAAGGAGAGGGAGGCCCATCACGAAGGCCACAATACCGTA 132

Qy  222 GACCTTACAGTCATAGAAGGCGCACCATTGCCTTTCGCTTACGATATCTTGACAACAGTA 281
        | |||| | ||  || |||| | ||||||||||| || |  |||||| | |  ||||||
Db  133 AAGCTTAAGGTAACCAAGGGTGGACCTTTGCCATTTGCTTGGATATTTGTCACCACAA   192

Qy  282 TTCGATTACGGCAACAGGGTATTCCCAAATACCCAGAGACATAGCAGATTATTCAAG 341
        |||  || | | || ||| ||| |  ||  ||| |||| ||  || ||| |||  |||
Db  193 TTTCAGTATGGAAGCAAGGTATATGTCAAGCACATACCAGACACTATAAAAAG       252

Qy  342 CAGACGTTTCCTGAGGGGTACTTCTGGGAACGAAGCATGCAGACGAAGACCAGGGCATT 401
        |||| |||||||||  |   | || |||     ||| ||| |  |   |||||||  |
Db  253 CTGTCATTTCCTGAAGGATTTAAATGGGAGAGGGTCATGAACTTTGAAGACGGTGGCGTC 312

Qy  402 TGCATCGCCACAAACGACATAACAATGATGGAAGGCGTCGACGACTGTTTGCCTATAAA 461
        || |  |  ||| |  |    | || |  | |||| | |  | | ||   |  ||||||
Db  313 GTTACTGTAACCCAGGATTCCAGTTTGCAGGATGG------CTGTTTCATCTTACAAG 363

Qy  462 ATTCGATTTGATGTGTGAACTTCCTGCCAATGTCCAGTTGTCAGAGGAAGACGCTG 521
        | ||||| | | || | |||  || || |  | |||| ||  |||| |  ||  |
Db  364 GTCAAGTTCATTGGGTGAACCTGTTGATGGACCTGTTATGCAAAAGAAGACAATG   423

Qy  522 AAATGGGAGCCATCCACTGAGATAATGTATGCGCCTGATGGAGTGCTGAAGGCTGATGTT 581
        ||| ||||  ||| |   |    | |||||| |  |||| | ||   |||| |||||| |
Db  424 GGCTGGGAAGCCAGCTGAGGATTTGTATCCTGTGATGGCGGTTGTTGTTGAAAAGATT   483

Qy  582 AACATGGCTCTGTTGCTTGAAGGAGGTGGCCATTACCGATGTGACTTCAAAACTACTTAC 641
        || | ||||  | | |  |    | ||| | |||  | |  | | ||| |||  ||||||
Db  484 CATAAGGCTCTGAAGCTGAAAGACGGTGGTCATTACCTAGTCGAATTCAAAAGTATTTAC 543

Qy  642 AAAGCTAAGAAGGTTGTCCGGTTGCCAGACTATCACTTTGTGGACCATCGCATGCGATT 701
        || |  |||| |||   |  |||| |||  ||| | | | |||  | ||| |||| |||
Db  544 ATGGCAAAGAAGCCTGTGCAGCTACCAGGGTACTACTATGTTGACTCCAAACTGGATATA 603

Qy  702 GTGAGCGCCACAGAAAGATTACAACAAGGTTAAGCTGCACAGCAGCATGCCGAAGCTCGTCAT 761
        ||||||| |||| ||||  | | | |||||||||||  ||| |  ||  | |||| |||||
Db  604 ACAAGCCACACACGAAGACTATACAAATCGTTGAGCAGTATGAAAGAACCGAGGGACGCCAC 663

Qy  762 GGACTGT 768
        |||||||
Db  664 CATCTGT 670
```

; FILE REFERENCE: 17084-022003 (420C)
; CURRENT APPLICATION NUMBER: US/11/082,154A
; CURRENT FILING DATE: 2005-03-15
; PRIOR APPLICATION NUMBER: 60/294,758
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: 60/366,891
; PRIOR FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: US 10/161,403
; PRIOR FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 876
; TYPE: DNA
; ORGANISM: Discosoma species
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (45)...(737)
; OTHER INFORMATION: Nucleotide sequence encoding red flourescent
; OTHER INFORMATION: protein (FP593)
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AF272711
; DATABASE ENTRY DATE: 2000-09-26
US-11-082-154A-39

Query Match   23.6%;   Score 252; DB 14;   Length 876;
Best Local Similarity   62.9%;   Pred. No. 7.3e-60;
Matches 428;   Conservative   0;   Mismatches 240;   Indels   12;   Gaps   2;

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Qy  102 AAGGGTGTGATTAAACCAGACATGAAGATGAAGCTGCGTATGGAAGGTGCTGTAAACGGG 161
        |||  ||||  | |||||||||||| ||||| |||||||||||||||||||| |||||||
Db   57 AAGAATGTGATCAAGGAGTTCATGAGGTTCAAGGTTCGTATGGAAGGAACCGTCATGGG  116

Qy  162 CACAAGTTCGTGGTTGAAGGAGATGAAAAGGGAAGCCTTTCGACCGAACACAGACTATG 221
        ||| ||||  | |  |||||| ||||| ||||||  ||  |  | || |||| |  |
Db  117 CACGAGTTTGAAATAAAAGGCGAAGGTGAGGGAAGTGTCACTGAGTGTCACTCACTGTTCCGTA 176

Qy  222 GACCTTACAGTCATAGAAGGCGCACCATTGCCTTTCGCTTACGATATCTTGACAACAGTA 281
        || ||| | || |||||| | ||||||||||||| ||||  |||||| | | | |||||
Db  177 AAGCTTATGGTAACCAAGGGTGGACCTTTGCCATTTGCTTTGATATTTTGTGATATTTTGTCACCACAA 236

Qy  282 TTCGATTACGGCAACAGGGTATTCCCAAATACCCAGAGACATAGCAGATTATTCAAG 341
        ||| ||| | | ||| |||| |  | | |  || | |||| ||  || ||| ||  |||
Db  237 TTTCAGTATGGAAGCAAGGTAAGGTATGAATTAAATGGAAAGGGATTTAAATGGGAGAGGGTCATGAACTTTGAAGA 296

Qy  342 CAGACGTTTCCTGAGGGGTACTTCTGGGAACGAAGCATGCAGACGAAGACCAGGGCATT 401
        | | |||||||||  |   | || ||||   |  | |||  | |  | | ||  | |||
Db  297 CTGTCATTTCCTGAGGGGGATTTAAATGGGAATTTAAATGGGAATTCATGAACTTTGA-- 356

Qy  402 TGCATCGCCACAAACGACATAACAATGATGGAAGGCGTCGACGACTGTTTGCCTATAAA 461
        || |  |  || | | |    || | |    | | | |   | | |||| ||  ||| |
Db  357 GTTACTGTATCCCAAGATTCCCAAGTTGA-------AAGACGGCTGTTTCATCTACGAG 407

Qy  462 ATTCGATTTGATGTGTGAACTTCCTGCCAATGTCCAGTTGTCAGAGGAAGACGCTG 521
        | ||||| |  ||   |||| ||||| | || | | || ||  |||| |||| ||
Db  408 GTCAAGTTCATTGGGTGAACTTCCTTCTGTTATGTATGCAGAGAGGACGGAAGACGCTG 467

Qy  522 AAATGGGAGCCATCCACTGAGATAATGTATGCGCCTGATGGAGTGCTGAAGGCTGATGTT 581
        ||||||||||| |  |  |  |  | |||| | || |||||||||||| |||||| | |
Db  468 GGCTGGGAAGCCAGCCAGCTCTGCGTTGTATCCTCGTGATGGGGTGCTGAAAGGAGGAGACATC 527

Qy  582 AACATGGCTCTGTTGCTTGAAGGAGGTGGCCATTACCGATGTGACTTCAAAACTACTTAC 641
        || |||| | || | ||||||| | |||||  ||||  | ||||| ||| || ||||||
Db  528 AACATGGCTCTGCCAGGTGAAGGAGGCGGCCATTACCGTTGTGACTTCAAGACTACTTAC 587

Qy  642 AAAGCTAAGAAGGTTGTCCGGTTGCCAGACTATCACTTTGTGGACCATCGCATGCGATT 701
        || | |||  ||||   | |  |||||||| ||  | |  | |  || ||| |||  ||
Db  588 ATGGTAAAGAAGCCTTCAGTTGCGTGCTGCCAGGCTACTATGTTGACTCCAAAACTGGAT 647

Qy  702 GTGAGCGCCACAGAAAGATTACAACAAGGTTAAGCTGCACAGCAGCATGCCGAAGCTCGT 758
        ||| ||| |||| ||||  | | | |  | |||| || |||| |||| | | |||||| |
Db  648 ATGACGAGCCACAACGAGATTACACAGTCGTTGAGCAGTATGAGAAAAAACCCAGGACGCGC 707
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RESULT 4
US-11-082-154A-39
; Sequence 39, Application US/11082154A
; Publication No. US20060024820A1
; GENERAL INFORMATION:
; APPLICANT: Perkins, Edward
; APPLICANT: Perez, Carl
; APPLICANT: Lindenbaum, Michael
; APPLICANT: Greene, Amy
; APPLICANT: Leung, Josephine
; APPLICANT: Fleming, Elena
; APPLICANT: Stewart, Sandra
; APPLICANT: Shellard, Joan
; TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS

Qy 759 CATGGACTGTCAAGGAAGGC 778
    || |||| || ||| ||||
Db 708 CACCATCCGTTCATTAAGCC 727

RESULT 5
US-11-100-988-4
; Sequence 4, Application US/11100988
; Publication No. US20060008878A1
; GENERAL INFORMATION:
; APPLICANT: Glick, Benjamin S.
; APPLICANT: Bevis, Brooke
; APPLICANT: Strongin, Daniel E.
; APPLICANT: Baker, David
; APPLICANT: Scalley-Kim, Michelle
; TITLE OF INVENTION: MONOMERIC RED FLUORESCENT PROTEINS
; FILE REFERENCE: 092234-9002-US01
; CURRENT APPLICATION NUMBER: US/11/100,988
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: US 60/560,340
; PRIOR FILING DATE: 2004-04-07
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
;
; SEQ ID NO 4
; LENGTH: 678
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: mutant red fluorescent protein DsRed.M1 based on Discosoma
; OTHER INFORMATION: species
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(678)
US-11-100-988-4

Query Match 21.6%; Score 230; DB 14; Length 678;
Best Local Similarity 60.6%; Pred. No. 9.1e-54;
Matches 399; Conservative 0; Mismatches 250; Indels 9; Gaps 1;

Qy 103 AGGGTGTGATTAAACCAGACATGAAGATGAAGCTGCGTATGGAAGGTGCTGTAAACGGGC 162
    ||| || || ||| |||||| ||| | ||| |||||| ||||||| ||| |||
Db 14 AGGACGTCATCAAGGAGTTCATGCAGTTCAAGGTGCGAGGGCTCCGTGAACGGCC 73

Qy 163 ACAAGTTCGTGGTTGAAGGAGATGGAAAAGGAAGCCTTTCGACGAACACAGACTATGG 222
    || |||| |||||| ||| | |||| |||| |||||| |||| ||| || ||
Db 74 ACTACTTCGAGATCGAGGGCGAGGGCGAGGGCAAGCCCTACGAGGGCACCCAGACACCGCCA 133

Qy 223 ACCTTACGAGTCATAGAAGGCGCACCATTGCCTTCGCTTACGATAATCTTGACACACAGTAT 282
    || | ||| | ||||| ||| ||||| || || ||| ||
Db 134 AGCTGCAGGTGACCAAGGGCGGCCCCCTGCCCTTCGCCTGGGACATCCTGTCCCCCCAGT 193

Qy 283 TCGATTACGGCAACAGGGTATTCGCCAAATACCCAGAGACAGACATAGCAGATTATTTCAAGC 342
    || ||||| || || |||| | |||| ||| ||| | ||
Db 194 TCCAGTACGGCCTCCAAGGCCTACGTGACCCAGGAGCGCACCCCGACCATGAACGAAGC 253

Qy 343 AGACGTTCCTGAGGGGTACTTCTGGGAACATGGGCATTT 402
    ||| |||||| ||| ||| |||||| ||||||
Db 254 TGTCCTTCCCCGGGAGGGCTTCACCTGGGAGCGCGTCATGAACTTCGAGGACGGCGGCGTGG 313

Qy 403 GCATCGCCACAAACGACTAACATGATGAAGACGCGTTCGACGACTGTTTGCCTATAAAA 462
    || |||| ||| || ||| ||| | |||| |
Db 314 TGGAGGTGCAGCAGGACTCCTCCCGAGGACGGCACC------TTCATCTACAAGG 364

Qy 463 TTCGATTGATGGTGTGAACTTTCTGCCAATGTCCAGTTATGCAGAGGAAGACGCTGA 522
    || ||||| || ||||||| |||||| || || |||||
Db 365 TGAAGTTCAAGGGCGTGAACTTCCCCGCCGACGGCCCCGTGATGCAGAAGAAGACTATGG 424

Qy 523 AATGGGAGGCCATCCACTGAGATAATGTATGCGCGTGAGTGAGTGGTGATGTTA 582
    ||||||| ||| |||| |||||| || |||||| |||||
Db 425 GCTGGGAGCCCTCCACCGAGAGGAGCGTGTCTGCTGGGGCGAGATCT 484

Qy 583 ACATGGCTCTGTTGTCTTGAAGGAGGTGGCCATTACCGATGTGACTTCAAAACTACTTACA 642
    || |||||| || || || ||||||
Db

Db 485 CCCACGCCCTGAGCTGAGGACGCGGCCACTACACCTGCGACTTCAAGACCGTGTACA 544
    || || ||||| ||

Qy 643 AAGCTAAGAAGGTTGTCCGGTTGCAGAGTATCACTTTGTGACCATCGGCATTGAGATTG 702
    ||||| |||||| | |||| |||| |||| ||
Db 545 AGGCCCAGAAGCCCGTGCAGCTGCCCGGCAACCACTACGTGGACTCCAAGCTGCAGCATCA 604

Qy 703 TGAGCCACGACAAAGATTACAACAAGGTTAAGCTGCACGAGCATGCCGAAGCTCGTCA 760
    | |||| |||| | ||||| || || | |||
Db 605 CCAACCAACCAACGAGGACTACACCGTGGTCGAGCAGTACGAGCACGCCGAGGCCGCCA 662

RESULT 6
US-11-208-927-1
; Sequence 1, Application US/11208927
; Publication No. US20060063229A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Yi
; APPLICANT: Falkowski, Paul
; TITLE OF INVENTION: mmPP encoding nucleic acids,
; TITLE OF INVENTION: polypeptides, antibodies and methods of use thereof
; FILE REFERENCE: Rutc.02-099US
; CURRENT APPLICATION NUMBER: US/11/208,927
; CURRENT FILING DATE: 2005-08-22
; PRIOR APPLICATION NUMBER: US/10/652,529
; PRIOR FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: 60/407,478
; PRIOR FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 3.0
;
; SEQ ID NO 1
; LENGTH: 645
; TYPE: DNA
; ORGANISM: Meandrina meandrites
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (329)...(329)
; OTHER INFORMATION: n= g or a
US-11-208-927-1

Query Match 21.2%; Score 226; DB 11; Length 645;
Best Local Similarity 62.8%; Pred. No. 1.2e-52;
Matches 409; Conservative 0; Mismatches 221; Indels 21; Gaps 3;

Qy 112 TTAAACCAGACATGAAGATGAAGCTGCGTATGGAAGGTGCTGTAAACGGGCACAAGTTCG 171
    || | || ||| || ||| | || |||| || ||
Db 8 TTCCAACGCAAGTGAAGATGAAGATGAAATATTCTATGGATGGCAACTTCAACGGCAGCTTTA 67

Qy 172 TGGTTGAAGGAGATGGAAAAGGAAGCCTTTCGACGAACACAGACTATGGACCTTACAG 231
    || |||| |||| || || |||| ||||| || || |||
Db 68 CTGTCGTAGGTGAAGGCACCGGCAATCCATACGAGGGCAATCAGTCGTTAAAACTCACCG 127

Qy 232 TCATAGAAGGCGCACCATTGCCTTTCGCTTACGATATCTTGACAGATTATTTCAAGC 291
    || | ||||| ||| || |||| || |
Db 128 TCA---AGGGCGAGCCCTCGCCTTTCGCGTTTGACATATTGTCAGCAACGTTCACTTATG 184

Qy 292 GCAACAGGGTATTCGCCAAATACCCAGAAGACATAGCAGATTATTTCAAGCAGACGTTTC 351
    |||| | ||| ||| ||| || ||||||
Db 185 GCAACAGGGTTTTTACTAAGTACCCTGAGGGAAACATGACATACGAGAGCACTATTTCAAGGAAGCATTTC 244

Qy 352 CTGAGGGGTACTTCTGGGAACATGGGCATTTGCATCGCCA 411
    ||||| ||| || | || |||| || || |||
Db 245 CTGGAGGGCTGACATGGGAAAGGACAATGACGTTCGAAGATGGCGCATTTGCACAGTCG 304

Qy 412 CAAACGACATAACAATGATGAAGACGCGTTCGACGACTGTTTTGCCTATAAAATTCGATTTG 471
    || || || ||| ||| | |||
Db 305 CAGCGGAAATAAGGCCTTACAGGAANCGTC-------TTCGAGCACAAATCCAAATTTG 355

Qy 472 ATGGTGTGAACTTTCCTGCCAATGGTCCAGTTATGCAGAGGAAGACGCTGAAATGGGAGC 531
    ||||||| || |||| |||| || || |||||| |||||||
Db 356 TCGGCGTGAACTTTCCCGCCAATGGACCTGTAATCCGTAATCCAGAAGAAGACGCGTTGGCTCGGAGA 415

Qy 532 CATCCACTGAGATAATGTATGCGCGTGATGAGTGAGTGGTCTGAAGGGTGATGTTAACATGGCTC 591
    ||||| |||| || | || |||
Db

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Db   416  CATCTACCGAGAAATGGCTGCCAACGATGATCCGTACAGGGCTATGTACCATGTTCC  475
          ||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Qy   592  TGTTGCTTGAGGAGGTGGCCATTACCGATGTGACTTCAAAACTACTTACAAAGCTAAGA  651
          ||||||||||||||||||||||||||||||||   ||| |||||||||
Db   476  TCAAGTGGAGGAGGTGGCCGTCACAAATGCTATTTCGTAACTAATCACAAAGCCAAA  535
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   652  AGGTTGTCCCGTTGCCAGACTATCACTTTGTGGACCATCGCATTGAGATTGTGAGCCACG  711
          ||  || |||||||||||||||||||||||||||||||
Db   536  GGGCCGTGAGGGTGCCAGATAACCATTTTGTGTGGCATCGCGTCCGTCGTTACG  591
          ||
Qy   712  ACAAAGATTACAACAACAAGGTTAAGTGCACGAGCATGCCGAAGCTCGTCATG  762
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   592  -----GATGGCAACACTGTTGAGCTGGAAGAAAACTGCAGAGAAGCTCGTTACG  637
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```
RESULT 7
US-10-209-208-5
; Sequence 5, Application US/10209208
; Publication No. US2005024921A1
; GENERAL INFORMATION:
;   APPLICANT: Tsien, Roger
;   APPLICANT: Campbell, Robert
;   APPLICANT: Baird, Geoffrey
;   TITLE OF INVENTION: FLUORESCENT PROTEIN VARIANTS AND METHODS
;   TITLE OF INVENTION: FOR MAKING SAME
;   FILE REFERENCE: UC083.1CP2CP2
;   CURRENT APPLICATION NUMBER: US/10/209,208
;   CURRENT FILING DATE: 2002-07-29
;   PRIOR APPLICATION NUMBER: 10/121,258
;   PRIOR FILING DATE: 2002-04-10
;   PRIOR APPLICATION NUMBER: 09/866,538
;   PRIOR FILING DATE: 2001-05-24
;   PRIOR APPLICATION NUMBER: 09/794,308
;   PRIOR FILING DATE: 2001-02-26
;   NUMBER OF SEQ ID NOS: 80
;   SOFTWARE: FastSEQ for Windows Version 4.0
;   SEQ ID NO 5
;   LENGTH: 678
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Polynucleotide encoding DsRed polypeptide variant
;   OTHER INFORMATION: "T1"
US-10-209-208-5

Query Match       21.0%;   Score 223.6;   DB 8;   Length 678;
Best Local Similarity   59.8%;   Pred. No. 5.6e-52;
Matches   398;   Conservative   0;   Mismatches   259;   Indels   9;   Gaps   1;
```

```
Qy   103  AGGGTGTGATTAAACCAGACATGAAGATGAAGATGAAGGTGCGTATGGAAGGTGCTGTAAACGGGGC  162
          ||| ||||| || |   | ||| ||||| ||||||||||||||||||| ||||||||||
Db    14  AGGACGTCATCAAGGAGTTCATGCGCTTCAAGGTGCGCATGGAGGGCTCCGTGAACGGCC  73
Qy   163  ACAAGTTCGTGGTTGAAGGAGATGGAAAAGGGAAGCCTTTCGACGGAACACAGACTATGG  222
          || |||||| ||| | || ||| ||| || ||||||  ||  ||||||| | | ||||
Db    74  ACGAGTTCGAGATCGAGGGCGAGGGCGAGGGCCGCCCCTACGAGGGCACCCAGACCGCCA  133
Qy   223  ACCTTACAGTCATAGAAGCGCACCATTGCCTTTCGCTTACGATATCTTGACAACAGTAT  282
          || | || | |  | ||  ||| ||| ||   ||  |||||||| ||| | |  |
Db   134  AGCTGAAGGTGACCAAGGGCGGCCTGCCCTTCGCCTGGGACATCCTGTCCCCCCAGT  193
Qy   283  TCGATTACGGCAACAGGGTATTCGCCAAATACCCAGAAGACATAGCAGATTATTTCAAGC  342
          |||||  || ||  || | ||||| |||  | ||  |  | |  ||   | |||||||
Db   194  TCCAGTACGGCTCCAAGGTGTACGTGAAGCACCCCGCCGACATCCCCGACTACAAGAAGC  253
Qy   343  AGACGTTTCCTGAGGGTACTTCTGGAACGAACGAGCGATGACATACGAGACCAGGGCATTT  402
          | | ||||   || ||| | | |||    |  |  | ||||| | | |  | ||
Db   254  TGTCCTTCCCCGAGGGCTTCAAGTGGGAGCGCGTGATGAACTTCGAGGACGGCGGCGTGG  313
Qy   403  GCATCGCCACAAACGACAGCATAACAATGATGAAGGCGTCGACGACTGTTTGCCTATAAA  462
          ||||   || ||   |||    | |  |  ||||   ||   ||
Db   314  TGACCGTGACCCAGGACTCCTCCCTGCAG-------GACGGCGCCTTCATCTACAAGG  364
```

```
Db   463  TTCGATTTGATGTGTGTGAACTTTCCTGCCAATGGTCCAGTTATGCAGAGGAGACGCTGA  522
          || ||| || | | || || |||| | || | ||| || ||| ||||| ||||  ||
Qy   365  TGAAGTTCATCGGCGTGAACTTCCCCGACGGCGTCCGTAATGCAGAAGAGACTATGG  424
Db   523  AATGGAGCCATCCACTGAGATAATGTATGCGGCCTGATGCGTGAAGGGTCTGATGTTA  582
          ||| ||   |||| |  |||  | || | | |  || | || | |  ||| ||||
Qy   425  GCTGGGAGGCCTCCACAGGAGTTGCTGTACCCCGACGGCGTGCTGAAGGGCGAGATCC  484
Db   583  ACATGGCTCTGTTGCTTGAAGGAGGTGGCCATTACGATGTGACTTCAAAACTACTTACA  642
          || ||||| || ||||| ||||| || || || |  ||| ||| |||||
Qy   485  ACAAGGCCCTGAAGCTGAAGGACGGCGGCCACTACCTGGTGGAGTTCAAGTCCATCTACA  544
Db   643  AAGCTAAGAAGGTTGTCCGGTTGCCAGACATCACTTTGTGGACCATCGCATTGAGATTG  702
          | || ||| ||| |||| |||| ||||| | ||  || ||| ||||| | || |||
Qy   545  TGGCCAAGAGCCCGTGCAGCTGCCCGGTCCGGTACGAGCTGAAGTCGAAGCTCGTCATG  604
Db   703  TGAGCCACGACAAAGATTACAACAAGGTTAAGTGCACGAGCATGCCGAAGCTCGTCATG  762
          ||||||  || |||||||||||| |||||||||||||||||||||| |||||||||||
Qy   605  CCTCCCAACGAGGACTACACCATCGTGGAGCAGTACGAGCGCGCCGAGGGCCGCCACC  664
Db   763  GACTGT  768
          |||||
Qy   665  ACCTGT  670
```

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RESULT 8
US-11-218-880-5
; Sequence 5, Application US/11218880
; Publication No. US20060003420A1
; GENERAL INFORMATION:
;   APPLICANT: Tsien, Roger
;   APPLICANT: Campbell, Robert
;   TITLE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT
;   TITLE OF INVENTION: PROTEIN VARIANTS AND METHODS FOR MAKING SAME
;   FILE REFERENCE: UC083.1CP2CP1
;   CURRENT APPLICATION NUMBER: US/11/218,880
;   CURRENT FILING DATE: 2005-09-01
;   PRIOR APPLICATION NUMBER: US/10/121,258
;   PRIOR FILING DATE: 2002-04-10
;   PRIOR APPLICATION NUMBER: 09/794,308
;   PRIOR FILING DATE: 2001-02-26
;   PRIOR APPLICATION NUMBER: 09/866,538
;   PRIOR FILING DATE: 2001-05-24
;   NUMBER OF SEQ ID NOS: 78
;   SOFTWARE: FastSEQ for Windows Version 4.0
;   SEQ ID NO 5
;   LENGTH: 678
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Polynucleotide encoding DsRed polypeptide variant
;   OTHER INFORMATION: "T1"
US-11-218-880-5

Query Match       21.0%;   Score 223.6;   DB 14;   Length 678;
Best Local Similarity   59.8%;   Pred. No. 5.6e-52;
Matches   398;   Conservative   0;   Mismatches   259;   Indels   9;   Gaps   1;
```

```
Qy   103  AGGGTGTGATTAAACCAGACATGAAGATGAAGATGCGGTATGGAAGGTGCTGTAAACGGGC  162
          ||| ||||| || |   | ||| ||||| ||||||||||||||||||| ||||||||||
Db    14  AGGACGTCATCAAGGAGTTCATGCGCTTCAAGGTGCGCATGGAGGGCTCCGTGAACGGCC  73
Qy   163  ACAAGTTCGTGGTTGAAGGAGATGGAAAAGGGAAGCCTTTCGACGGAACAGACTATGG  222
          || |||||| ||| | || ||| ||| || ||||||  ||  ||||||| | ||||
Db    74  ACGAGTTCGAGATCGAGGGCGAGGGCGAGGGCCGCCCCTACGAGGGCACCCAGACCGCCA  133
Qy   223  ACCTTACAGTCATAGAAGCGCACCATTGCCTTTCGCTTACGATATCTTGACAACAGTAT  282
          || | || | |  | ||  ||| ||| ||   ||  |||||||| ||| | |  |
Db   134  AGCTGAAGGTGACCAAGGGCGGCCTGCCCTTCGCCTGGGACATCCTGTCCCCCCAGT  193
Qy   283  TCGATTACGGCAACAGGGTATTCGCCAAATACCCAGAAGACATAGCAGATTATTTCAAGC  342
          |||||  || ||  || | ||||| |||  | ||  |  | |  ||   | |||||||
Db   194  TCCAGTACGGCTCCAAGGTGTACGTGAAGCACCCCGCCGACATCCCCGACTACAAGAAGC  253
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RESULT 9
US-11-187-622-7
; Sequence 7, Application US/11187622
; Publication No. US2006035330A1
; GENERAL INFORMATION:
; APPLICANT: Lukyanov, Sergey
; APPLICANT: Lukyanov, Konstantin
; APPLICANT: Yanushevich, Yuriy
; APPLICANT: Savistky, Alexandr
; APPLICANT: Fradkov, Arcady
; TITLE OF INVENTION: Non Aggregating Fluorescent Proteins and
; TITLE OF INVENTION: Methods for Using the Same
; FILE REFERENCE: CLON-067
; CURRENT APPLICATION NUMBER: US/11/187,622
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/081,864
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: 10/006,922
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/270,983
; PRIOR FILING DATE: 2001-02-21
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 678
; TYPE: DNA
; ORGANISM: Discosoma sp
US-11-187-622-7

Query Match   20.6%;   Score 219.8;   DB 11;   Length 678;
Best Local Similarity   59.4%;   Pred. No. 6.4e-51;
Matches   396;   Conservative   0;   Mismatches 262;   Indels 9;   Gaps   1;

```
Qy  343 AGACGTTTCCTGAGGGGTACTTCTGGGAACGAAGCATGACATACGAAGACCAGGGCATTT 402
            || | |||||||||  |  |||  |||||    |||
Db  254 TGTCCTTCCCGAGGGCTTCAAGTGGGAGGCGCGTGATGAACTTCGAGGACGGCGCGTGG 313

Qy  403 GCATCGCCACAAACGACATAACAATGATGGAAGGCGTGACGACTGTTTTGCCTATAAAA 462
            || || ||| ||   |         ||||      |||
Db  314 TGACCGTGACCCGAGGACTCCTCCCTGCAG--------GACGGCTGCTTCATCTACACAGG 364

Qy  463 TTCGATTTGATGGTGTGAACTTCCTGCCAATGGTCCAGTTATGCAGAGGAAGACGCTGA 522
        || ||||| || |||||||||||||   |   ||| |||  |||||||  ||
Db  365 TGAAGTTCATCGGCGTGAACTTCCCCGTCCGCAGCGGCCCCGTAATGCAGAGAGACTATGG 424

Qy  523 AATGGGAGCCATCCACTGAGATAATGTATGCGCCTGATGGAGTGCTGAAGGGTGATGTTA 582
         ||||||| |||| ||| || |   |||    | |||| |||||||||||| ||
Db  425 GCTGGGAGGCCTTCACCGAGCGGGTGTACCCCCGCGACGGCGTGCTGCTGAAGGGCGAGATCC 484

Qy  583 ACATGGCTCGTGTTGCTTGAAGGAGGTGGCCATTACCGATGTGACTTCAAAACTACTTACA 642
        ||| || | |   ||||| ||||  |  |||||||| ||||||||| ||||| ||||| ||
Db  485 ACAAGGGCCTGAAGCTGAAGGACGGCGCGCCCACTACCTGGGAGTTCAAGTCCATCTACA 544

Qy  643 AAGTAAGAAGGTTGTCCGGTTGCGACTATCACTTTGTGGACCATCGCATTGAGATTG 702
        ||| | |||||  |||| || |  |||||||| ||||||||| | | | |||||
Db  545 TGGCCAAGAAGCCCGTGCAGCTGCCCGGCTACTACTACGTGGACTCCAAGCTGGACATCA 604

Qy  703 TGAGCCACGACAAAGATTACAACAAGGTTAAGCTGCACGAGCATGCCGAGCTCGTCATG 762
        || ||||||||||||||||||||||| || ||||| |||||||||||||| || |
Db  605 CCTCCCACAACGAGGACTACACCATCGTGGAGCAGTACGAGCGCGCCCGAGGGGCCGCCACC 664

Qy  763 GACTGT 768
            |||||
Db  665 ACCTGT 670
```

RESULT 10
US-10-209-208-3
; Sequence 3, Application US/10209208
; Publication No. US20050244921A1
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger
; APPLICANT: Campbell, Robert
; APPLICANT: Baird, Geoffrey
; TITLE OF INVENTION: FLUORESCENT PROTEIN VARIANTS AND METHODS
; TITLE OF INVENTION: FOR MAKING SAME
; FILE REFERENCE: UC083.1CP2CP2
; CURRENT APPLICATION NUMBER: US/10/209,208
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: 10/121,258
; PRIOR FILING DATE: 2002-04-10
; PRIOR APPLICATION NUMBER: 09/866,538
; PRIOR FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 09/794,308
; PRIOR FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 681
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: nucleotide sequence encoding DsRed with mammalian
; OTHER INFORMATION: codon usage
US-10-209-208-3

```
Db   73 CACGAGTTCGAGATCGAGGGCGAGGGCGAGGGCCGCCCCTACGAGGGCCACAACACCGTG 132

Qy  222 GACCTTACAGTCATAGAAGGCGCACCATTGCCTTTGCCTTACGATATCTTGACAACAGTA 281
         |||||| || || |||||||| |||| | |||| |||||| |  || ||||
Db  133 AAGCTGAAGGTGACCAAGGGCGGCCCCCTGCCCTTCGCCTGGGACATCCTGTCCCCCCAG 192

Qy  282 TTCGATTACGGCAACACGGGTATTCGCCAAATACCAGAAGACATAGCAGATTATTCAAG 341
        |||| ||||||| ||| ||||| |    || |||| |||||||| ||||| |  |||||
Db  193 TTCCAGTACGGCTCCAAGGTGTACGTGAAGCACCCCGCAGACATCCCCGACTACAAGAAG 252

Qy  342 CAGACGTTTCCTGAGGGGTACTTCTGGGAACGAAGCATGACATACGAAGACCAGGGCATT 401
        | ||| || |||||||||||  |||||||  | ||||||| || || |||
Db  253 CTGTCCTTCCCCGAGGGGTTCAAGTGGGAGCGCGTGATGAACTTCGAGGACGGCGCGTG 312

Qy  402 TGCATCGCCACAAACGACATAACAATGATGGAAGGCGTGACGACTGTTTTGCCTATAAA 461
         ||| || ||| ||   |         ||||      |||
Db  313 GTGACCGTGACCCAGGACTCCTCCCTGCAG--------GACGGCTGCTTCATCTACAAG 363

Qy  462 ATTCGATTTGATGGTGTGAACTTCCTGCCAATGGTCCAGTTATGCAGAGGAAGAGCGTG 521
        ||| ||||| || |||||||||||||   |   ||| |||  |||||||  |||
Db  364 GTGAAGTTCATCGGCGTGAACTTCCCCGTCCGACGGCGCCCGTGATGCAGAGAAGAGACCATG 423

Qy  522 AAATGGGAGCCATCCACTGAGATAATGTATGCGCCTGATGGAGTGCTGAAGGGTGATGTT 581
          ||||||| |||| ||| || |   |||    | |||| |||||||||||| ||
Db  424 GGCTGGGAGGCCTTCACCGAGCGGGTGTACCCCCGCGACGGCGTGCTGCTGAAGGGCGAGATC 483

Qy  582 AACATGGCTCGTGTTGCTTGAAGGAGGTGGCCATTACCGATGTGACTTCAAAAACTACTTAC 641
        ||| || | |   ||||| ||||  |  |||||||| ||||||||| |||||| ||||| ||
Db  484 CACAAGGGCCTGAAGCTGAAGGACGGCGGCCCACTACCTGGTGGAGTTCAAGTCCATCTAC 543

Qy  642 AAAGCTAAGAAGGTTGTCCGGTTGCCAGACTATCACTTTGTGACCATCGCATTGAGATT 701
        ||| | |||||  |||| || ||  |||||||| ||||||||| | | | |||||
Db  544 ATGGCCAAGAAGCCCGTGCAGCTGCCCGGCTACTACTACGTGGACTCCAAGCTGGACATC 603

Qy  702 GTGAGCCACGACAAAGATTACAACAAGGTTAAGCTGCACGAGCATGCCGAGCTCGTCAT 761
        || ||||||||||||||||||||||| || ||||| |||||||||||||| || |
Db  604 ACCTCCCACAACGAGGACTACACCATCGTGGAGCAGTACGAGCGCGCCGAGGGGCCGCCAC 663

Qy  762 GGACTGT 768
            |||||
Db  664 CACCTGT 670
```

```
Qy  102 AAGGGTGTGATTAAACCAGACATGAAGATGAAGCTGCGTATGGAAGGTGCTGTAAACGGG 161
        ||||| || || ||  ||||||| |||||||| || ||  ||||| |||| | |||||||
Db   13 AAGAACGTCATCAAGGAGTTCATGCGCTTCAAGGTGCGCATGGAGGGCACCGTGAACGGC 72

Qy  162 CACAAGTTCGTGGTTGAAGGAGATGGAAAAGGAGAAAGGCCTTTCGACGAACACAGACTATG 221
        ||||||||||| || ||||||| || || | || || ||||  |||| ||| | |
```

RESULT 11 (left column)

```
Query Match        20.6%;   Score 219.8;  DB 8;   Length 681;
Best Local Similarity  59.4%;  Pred. No. 6.4e-51;
Matches 396;  Conservative  0;  Mismatches 262;  Indels  9;  Gaps  1;

Qy  102 AAGGGTGTGATTAAACCAGACATGAAGATGAAGCTGCGTATGGAAGGTGTGTAAACGGG 161
            ||||  ||  ||  ||  || ||  ||  ||   |   ||  |||||
Db   16 AAGAACGTCATCAAGGAGTTCATGCGCTTCAAGGTGCCATGGAGGGCACCGTGAACGGC 75
Qy  162 CACAAGTTCGTGGTTGAAGGAGATGAAAAGGGAAGCCTTTCGACGGAACACAGACTATG 221
        ||| ||||||    | |  |||  | |  || |   | ||| || ||
Db   76 CACGAGTTCGAGATCGAGGGCGAGGGCGAGGGCCGCCCCTACGAGGGCACCCAGACCGTG 135
Qy  222 GACCTTACAGTCATAGAAGCGCACCATTGCCTTTCGCTTACGATATCTTGACAACAGTA 281
        |   | ||  |  ||    || |   | |||||||||| ||  || |  |
Db  136 AAGCTGAAGGTGACCAAGGGCGGCCCCCTGCCCTTCGCCTGGGACATCCTGTCCCCCAG 195
Qy  282 TTCGATTACGGCAACAGAGGGTATTCGCCAAATACCCAGACACATAGCAGATTATTTCAAG 341
        ||| |||ACGGC||    | || || ||   |   | ||  || || ||    |||||
Db  196 TTCCAGTACGGCTCCAAGGTGTACGTGAAGCACCCCGCCGACATCCCGACTACAAGAAG 255
Qy  342 CAGACGTTTCTGAGGGGTACTTCTCGGGAACGAAGCATGCATACGAAGACCAGGGCATT 401
        |   | ||| |GAGGG  || ||  |    || | ||   |  |GAAGACCAGGG|||
Db  256 CTGTCCTTCCCCGAGGGCTTCAAGTGGGAGCGCGTGATGAACTTCGAGGACGGCGGCGTG 315
Qy  402 TGCATCGCCACAAACGACATAACAATGATGGAAGGCGTCGACGACTGTTTTGCCTATAAA 461
        ||  | |   ||    |       | ||| |     |  |GACGGCGTG||| | |||
Db  316 GTGACCGTGACCCAGGACTCCTCCCTGCAG--------GACGGCGTGCTTCATCTACAAG 366
Qy  462 ATTCGATTTGATGGTGTGAACTTTCCTGCCAATGGTCCAGTTATGCAGAGGAAGACGCTG 521
         ||  | || | |GTGTGAAC|| || |   | |  ||  |||GCAGA  AAGACC||
Db  367 GTGAAGTTCATCGGCGTGAACTTCCCCTCCGACGGCCCCGTAATGCAGAAGAAGACCATG 426
Qy  522 AAATGGGAGCCATCCACTGAGATAATGTATGCGCGTGAGGTGCTGAAGGGTGATGTT 581
         | TGGGAGCC|TCCAC GAG       | |  |||  || ||CTGAAGGG GA
Db  427 GGCTGGGAGGCCTCCACCGAGCGCGTGACCCCCGACGGCGTGCTGAAGGGCGAGATC 486
Qy  582 AACATGGCTCTGTTGCTTGAAGGAGGTGGCCATTACCGATGTGACTTCAAAACTACTTAC 641
         ACA GGC CTG  GCTGAAGG GGCGGCCA TAC   TG  | ||CAA   | CATCTAC
Db  487 CACAAGGCCCTGAAGCTGAAGGACGGCGGCCACTACCTGTGGAGTTCAAGTCAGTCCATCTAC 546
Qy  642 AAAGCTAAGAAGGTTGTCCGGTTGCCAGACTATCACTTTGTGAACCATCCGCCATTGAGATT 701
         | GCCAAGAAG   GT CGG | GCC GACTA TACTA GTGGAC  CAAGCTGGACATC
Db  547 ATGGCCAAGAAGCCCGTGCAGCTGCCCGGCTACTACTACGTGGACTCCAAGCTGGACATC 606
Qy  702 GTGAGCCACGACAAAGATTACAACAAGGTTAAGCTGCACAAGACATGCCGAGCCTCGTCAT 761
         |  | CAC A  |  GATTACAAC | GT AAGCTGCACAAGAC  GCCGAGCC  C C  |
Db  607 ACCTCCCACAACGAGGACTACACCATCGTGGAGCAGTACGAGCGCCACCGAGGGCCGCCAC 666
Qy  762 GGACTGT 768
        ||||
Db  667 CACCTGT 673
```

RESULT 11
US-10-209-208-23
; Sequence 23, Application US/10209208
; Publication No. US2005024921A1
GENERAL INFORMATION:
; APPLICANT: Tsien, Roger
; APPLICANT: Campbell, Robert
; APPLICANT: Geoffrey Baird
; TITLE OF INVENTION: FLUORESCENT PROTEIN VARIANTS AND METHODS
; TITLE OF INVENTION: FOR MAKING SAME
; FILE REFERENCE: UC083.1CP2CP2
; CURRENT APPLICATION NUMBER: US/10/209,208
; CURRENT APPLICATION FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: 10/121,258
; PRIOR APPLICATION FILING DATE: 2002-04-10
; PRIOR APPLICATION NUMBER: 09/866,538
; PRIOR APPLICATION FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 09/794,308
; PRIOR APPLICATION FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 80

RESULT 12 (right column)

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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 681
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: nucleotide sequence encoding DsRed with mammalian
; OTHER INFORMATION: codon usage
US-10-209-208-23

Query Match        20.6%;   Score 219.8;  DB 8;   Length 681;
Best Local Similarity  59.4%;  Pred. No. 6.4e-51;
Matches 396;  Conservative  0;  Mismatches 262;  Indels  9;  Gaps  1;

Qy  102 AAGGGTGTGATTAAACCAGACATGAAGATGAAGCTGCGTATGGAAGGTGTGTAAACGGG 161
Db   16 AAGAACGTCATCAAGGAGTTCATGCGCTTCAAGGTGCCATGGAGGGCACCGTGAACGGC 75
Qy  162 CACAAGTTCGTGGTTGAAGGAGATGAAAAGGGAAGCCTTTCGACGGAACACAGACTATG 221
Db   76 CACGAGTTCGAGATCGAGGGCGAGGGCGAGGGCCGCCCCTACGAGGGCACCCAGACCGTG 135
Qy  222 GACCTTACAGTCATAGAAGCGCACCATTGCCTTTCGCTTACGATATCTTGACAACAGTA 281
Db  136 AAGCTGAAGGTGACCAAGGGCGGCCCCCTGCCCTTCGCCTGGGACATCCTGTCCCCCAG 195
Qy  282 TTCGATTACGGCAACAGAGGGTATTCGCCAAATACCCAGACACATAGCAGATTATTTCAAG 341
Db  196 TTCCAGTACGGCTCCAAGGTGTACGTGAAGCACCCCGCCGACATCCCGACTACAAGAAG 255
Qy  342 CAGACGTTTCTGAGGGGTACTTCTCGGGAACGAAGCATGCATACGAAGACCAGGGCATT 401
Db  256 CTGTCCTTCCCCGAGGGCTTCAAGTGGGAGCGCGTGATGAACTTCGAGGACGGCGGCGTG 315
Qy  402 TGCATCGCCACAAACGACATAACAATGATGGAAGGCGTCGACGACTGTTTTGCCTATAAA 461
Db  316 GTGACCGTGACCCAGGACTCCTCCCTGCAG--------GACGGCGTGCTTCATCTACAAG 366
Qy  462 ATTCGATTTGATGGTGTGAACTTTCCTGCCAATGGTCCAGTTATGCAGAGGAAGACGCTG 521
Db  367 GTGAAGTTCATCGGCGTGAACTTCCCCTCCGACGGCCCCGTAATGCAGAAGAAGACCATG 426
Qy  522 AAATGGGAGCCATCCACTGAGATAATGTATGCGCGTGAGGTGCTGAAGGGTGATGTT 581
Db  427 GGCTGGGAGGCCTCCACCGAGCGCGTGACCCCCGACGGCGTGCTGAAGGGCGAGATC 486
Qy  582 AACATGGCTCTGTTGCTTGAAGGAGGTGGCCATTACCGATGTGACTTCAAAACTACTTAC 641
Db  487 CACAAGGCCCTGAAGCTGAAGGACGGCGGCCACTACCTGTGGAGTTCAAGTCAGTCCATCTAC 546
Qy  642 AAAGCTAAGAAGGTTGTCCGGTTGCCAGACTATCACTTTGTGAACCATCCGCCATTGAGATT 701
Db  547 ATGGCCAAGAAGCCCGTGCAGCTGCCCGGCTACTACTACGTGGACTCCAAGCTGGACATC 606
Qy  702 GTGAGCCACGACAAAGATTACAACAAGGTTAAGCTGCACAAGACATGCCGAGCCTCGTCAT 761
Db  607 ACCTCCCACAACGAGGACTACACCATCGTGGAGCAGTACGAGCGCCACCGAGGGCCGCCAC 666
Qy  762 GGACTGT 768
Db  667 CACCTGT 673
```

RESULT 12
US-11-218-880-3
; Sequence 3, Application US/11218880
; Publication No. US20060003420A1
GENERAL INFORMATION:
; APPLICANT: Tsien, Roger
; APPLICANT: Campbell, Robert
; TITLE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT
; TITLE OF INVENTION: PROTEIN VARIANTS AND METHODS FOR MAKING SAME
; FILE REFERENCE: UC083.1CP2CP1

CURRENT APPLICATION NUMBER: US/11/218,880
CURRENT FILING DATE: 2005-09-01
PRIOR APPLICATION NUMBER: US/10/121,258
PRIOR FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 78
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 681
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: nucleotide sequence encoding DsRed with mammalian
OTHER INFORMATION: codon usage
US-11-218-880-3

Query Match   20.6%; Score 219.8; DB 14; Length 681;
Best Local Similarity   59.4%; Pred. No. 6.4e-51;
Matches 396; Conservative   0; Mismatches 262; Indels   9; Gaps   1;

Qy   102 AAGGGTGATTAAACCAGACATGAAGATGAAGCTGCGTATGGAAGGTGCTGTAAACGGG 161
          || || || ||| ||||| || |||||| ||| || ||||||
Db   16 AAGAACGTCATCAAGGAGTTCATGCGCTTCAAGGTGCCATGGAGGGCACCGTGAACGGC 75

Qy   162 CACAAGTTCGTGGTTGAAGGAGATGGAAACAGGGAAGCCTTTCGACGGAACACAGACTATG 221
          ||| |||||| | | ||| |||||| | || || | ||
Db   76 CACGAGTTCGAGATCGAGGGCGAGGGCGAGGGCCGCCCCTACGAGGGCCACACCGTG 135

Qy   222 GACCTTACAGTCATAGAAGGGCCACCATTGCCTTTCGCTTACGATATCTTGACAACAGTA 281
          | || || || || || |||||||| ||||||| || | ||| ||| ||
Db   136 AAGCTGAAGGTGACCAAGGGCGGCCCCCTGCCCTTCGCCTGGGACATCCTGTCCCCCAG 195

Qy   282 TTCGATTACGGCAACAGGGTATTCGCCAAATACCCAGAAGACATAGCAGATTATTCAAG 341
          ||| | ||||| | ||| | ||| || ||| ||| | ||| || | || ||||
Db   196 TTCCAGTACGGCTCCAAGGTGTACGTGAAGCACCCCGCCGACATCCCGACTACAAGAAG 255

Qy   342 CAGACGTTTCCTGAGGGGTACTTCGGGAACGAAGACATGACATGACAGGGCATT 401
          ||||| | || |||| | ||||| ||| | |||| ||| || ||
Db   256 CTGTCCTTCCCCGAGGGCTTCAAGTGGGAGCGCGTGATGAATGAACTTCGAGGACGGCGGCGTG 315

Qy   402 TGCATCGCCACAAACGACATAACAATGATGAAGGCGTCGACGACTGTTTTGCCTATAAA 461
          ||| || ||||| ||| || || ||||||| | ||| || || | ||| || |
Db   316 GTGACCGTGACCCAGGACTCCTCCCTGCAG-------GACGGCGTGCTTCATCTACAAG 366

Qy   462 ATTCGATTTGATGGTGTGAACTTCCTGCCAATGGTCCAGTTATGCGACGAAGACGCGTG 521
          || || | || | |||||||||| | || | || ||| || | || || ||| ||
Db   367 GTGAAGTTCATCGGCGTGAACTTCCCCTCCGACGGCCCGTAATGCAGAAGAACCATG 426

Qy   522 AAATGGGAGCCATCCACTGAGATAATGTATGCGCGTGATGAGTGCTGAAGGGTGATGTT 581
          | | ||||| || || || || | | | || | ||||| || ||||| |||| ||
Db   427 GGCTGGGAGGCCTCCACCGAGAGGTTGCACGAGGCCCTGAAGGGCGAGATC 486

Qy   582 AACATGGCTCTGTTGCTTGAAGGAGGTGGCCATTACCGATGTGACTTCAAAACTACTTAC 641
          || ||||| ||| | || |||| ||| |||| |||| | ||| ||||| ||| ||
Db   487 CACAAGGCCCTGAAGCTGAAGGACGGCGGCCACTACGACGCCGAGGTGAAGTTCATCTACTAC 546

Qy   642 AAAGCTAAGAAGGTTGTCCGGTTGCCAGCTATCACTTTGTGACCATCGCATTGAGATT 701
          || || ||| | || | || || | || || || | ||| || | | ||| || |
Db   547 ATGGCCAAGAGCAGCCCGTGCAGCTGACTGGACTCCAAGCTGGACATC 606

Qy   702 GTGAGCCACGACAAAGATTACACACAAGGTTAAGCTGCACGAGCATGCCGAAGCTCGTCAT 761
          ||||| || || || |||||||| |||| ||| ||||||| ||| | || |||| ||
Db   607 ACCTCCACACGAGGACTACACCATCGTGGAGCAGTACGAGCGCGCACCGAGGGCCGCCAC 666

Qy   762 GGACTGT 768
          |||||
Db   667 CACCTGT 673

RESULT 13

```
Db    607 ACCTCCCACAACGAGGACTACACCATCGTGGAGCAGTACGAGCGCCACCGAGGGCCGCCAC 666
          ||||  ||  ||    |||| |||  ||| |||||||| |||||  || ||| |||| ||||
Qy    762 GGACTGT 768
          |||||
Db    667 CACCTGT 673
```

RESULT 14
US-11-082-154A-29
; Sequence 29, Application US/11082154A
; Publication No. US2006024820A1
GENERAL INFORMATION:
; APPLICANT: Perkins, Edward
; APPLICANT: Perez, Carl
; APPLICANT: Lindenbaum, Michael
; APPLICANT: Greene, Amy
; APPLICANT: Leung, Josephine
; APPLICANT: Fleming, Elena
; APPLICANT: Stewart, Sandra
; APPLICANT: Shellard, Joan
; TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
; FILE REFERENCE: 17084-022003 (420C)
; CURRENT APPLICATION NUMBER: US/11/082,154A
; CURRENT FILING DATE: 2005-03-15
; PRIOR APPLICATION NUMBER: 60/294,758
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: 60/366,891
; PRIOR FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: US 10/161,403
; PRIOR FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 4692
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pDSred1-N1 plasmid from Clontech
US-11-082-154A-29

```
Query Match       20.6%;  Score 219.8;  DB 14;  Length 4692;
Best Local Similarity  59.4%;  Pred. No. 1.6e-50;
Matches  396;  Conservative  0;  Mismatches 262;  Indels 9;  Gaps 1;

Qy    102 AAGGGTGTGATTAAACCAGACATGAAGATGAAGAGTGCGTATGGAAGGTGCTGTAAACGGG 161
          ||  | ||    ||  | || ||||| ||  || ||  ||||||||| ||| |||||||||
Db    694 AAGAACGTCATCAAGGAGTTCATGCGCTTCAAGGTGCGCATGGAAGGCCACCGTGAACGGC 753

Qy    162 CACAAGTTCGTGGTTGAAGGAGATGGAAAAGGAAGCCTTCGACGGAACACAGACTATG 221
          ||| |||||| |  | |||||  |||| | ||  || || ||||| || || ||  |||
Db    754 CACGAGTTCGAGATCGAGGGCGAGGGCGAGGGCCGCCCCTACGAGGGCCACACCCGTG 813

Qy    222 GACCTTACAGTCATAGAAGGCGCACCATTGCCTTTCGCTTCACGATATCTTGACAACAGTA 281
          | || ||  || |    |||||| |  || ||||| || |  |  |||| |||   |||
Db    814 AAGCTGAAGGTGACCAAGGGCGGCCCCCTGCCCTTCGCCTGGGACATCCTGTCCCCCAG 873

Qy    282 TTCGATTACGGCAACAGGGTATTCGCCAAATACCCAGAGACATAGCAGATTATTTCAAG 341
          ||| | |||||| ||| ||||||| || |  ||  | |  || ||| |  ||  |||| ||
Db    874 TTCCAGTACGGCTCCAAGGTGTACGTGAAGCACCCCGCCGACATCCCCGACTACAAGAAG 933

Qy    342 CAGACGTTTCCTGAGGGGTTACTTCTGGGAACGATGACATGAAGCATGAAGACCAGGGCATT 401
          | | |  || || || |  | |  |  |||  || |  ||||| ||| |||| |||||| ||
Db    934 CTGTCCTTCCCCGAGGGCTTCAAGTGGGAGCGCGTGATGAACTTCGAGGACGGCGGCGTG 993

Qy    402 TGCATCGCCACAAACGACATAACAATGATGGAAGGCGTCGACGACTGTGTTTGCCTATAAA 461
          |||| ||||||||| ||||  | ||| | ||| || |  || || || ||||| | ||
Db    994 GTGACCGTGACCCAGGACTCCTCCCTGCAG-------GACGGCTGCGTCAATCTACACAAG 1044

Qy    462 ATTCGATTTGATGGTGTGAACTTTCCTGCCAAATGTCCAGTTACGGAGAAGACGCTG 521
          || ||||| || || |||||||| || | |  | ||||||| | |||| ||||  |||
Db    1045 GTGAAGTTCATCGGCGTGAACTTCCCCTCCGACGGCCCCGTAATGCAGAAGAGACCCATG 1104
```

```
Db    522 AAATGGGAGCCATCCACTGAGATAATGTATGCGGTGATGGAGTGCTGAAGGGTGATGTT 581
          ||  ||||| |||||| ||| ||  || ||| | ||||| ||| |||||||| || ||
Db    1105 GGCTGGGAGGGCTCCACCGAGCGCGTGTACCCCCGACGGCGTGCTGAAGGGCGAGATC 1164

Qy    582 AACATGGCTCTTGTTGCTTGAAGGAGGTGGCCATTACCGATGTGACTTCAAAACTACTTAC 641
          ||||| || ||| |||  |||||| |||| ||| |||| ||||| ||||||  | ||  ||
Db    1165 CACAAGGCCCTGAAGCTGAAGGACGGCGGCCACTACCTGGTCGAGTTCAAGTCATCATCTAC 1224

Qy    642 AAAGCTAAGAAGGTTGTCCGGTTGCGACGATCACTTGTGTGGACCATTGCCATTGAGATT 701
          ||||| |||||| | || ||| |||| | || |||  || |||| || ||| || ||| ||
Db    1225 ATGGCCAAGAAGAGCCCGTGCAGCTGCCGGCTACTACTACGTGGACTCCAAGTGGACATC 1284

Qy    702 GTGAGCCACGACAAAGATTACAACAAGGTTAAGTCGACGAGCATGCGCAAGCTCGTCAT 761
          || || ||||||||  |||| |||||| || |||  |||| || ||||||| || |||
Db    1285 ACCTCCCACAACGAGGACTACACCATCGTGGAGCAGTACGAGCAGTACGAGCGCCACCGAGGGCCGCCAC 1344

Qy    762 GGACTGT 768
          |||||
Db    1345 CACCTGT 1351
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RESULT 15
US-11-187-622-13
; Sequence 13, Application US/11187622
; Publication No. US2006003530A1
GENERAL INFORMATION:
; APPLICANT: Lukyanov, Sergey
; APPLICANT: Lukyanov, Konstantin
; APPLICANT: Yanushevich, Yuriy
; APPLICANT: Savitsky, Alexandr
; APPLICANT: Fradkov, Arcady
; TITLE OF INVENTION: Non-Aggregating Fluorescent Proteins and
; TITLE OF INVENTION: Methods for Using the Same
; FILE REFERENCE: CLON-067
; CURRENT APPLICATION NUMBER: US/11/187,622
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/081,864
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: 10/006,922
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/270,983
; PRIOR FILING DATE: 2001-02-21
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 675
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: non-aggregating mutant
US-11-187-622-13

```
Query Match       20.2%;  Score 215.8;  Pred. No. 8.4e-50;  DB 11;  Length 675;
Best Local Similarity  59.7%;
Matches  386;  Conservative  0;  Mismatches 252;  Indels 9;  Gaps 1;

Qy    122 CATGAAGATGAAGAGTGCGTATGGAAGGTGCTGTAAACGGGCACAAGTTCGTGGTTGAAGG 181
          |||| ||  || ||  ||||||||| ||| |||||||||| ||| |||||| |  | |||||
Db    33  CATGCGCTTCAAGGTGCGCATGGAAGGCCACCGTGAACGGCCACGAGTTCGAGATCGAGGG 92

Qy    182 AGATGGAAAAGGGAAGCCTTTCGACGGAACACAGACTATGGACCTTACAGTCATAGAAGG 241
          | ||||| | ||  || || ||||| || || ||  ||| | || ||  || |    |||
Db    93  CGAGGGCGAGGGCGAGGGCCGCCCCTACGAGGGCCACACCCGTGAAGCTGAAGGTGACCAAGGG 152

Qy    242 CGCACCATTGCCTTTCGCTTCACGATATCTTGACAACAGTATTCGATTACGGCAACAGGGT 301
          |||| |  || ||||| || |  |  |||| |||   || ||| | ||||||| ||| |||
Db    153 CGGCCCCCTGCCCTTCGCCTGGGACATCCTGTCCCCCAGTTCCAGTACGGCTCCAAGGT 212

Qy    302 ATTCGCCAAATACCCAGAGACATAGCAGATTATTTCAAGCAGACGTTTCCTGAGGGGGTA 361
          ||| | |  ||  | |  || || ||| |  ||  |||| | |  || || || |  |
Db    213 GTACGTGAAGCACCCCGCCGACATCCCCGACTACAAGAAGCTGTCCTTCCCCGAGGGCTT 272

Qy    362 CTTCTGGGAACGATGACATCAGAAGACATACGAGAAGACCAGGGCATTTGCATCGCCACAAAGACAT 421
```

```
Db      273 ―――――――――――― |||||| ||      |||| ||    |  |||| ||| | ||||
            CAAGTGGGAGCGCCGTGATGAACTTCGAGGACGGCGGCGTGCGCGACCGTGACCCAGGACTC 332

Qy      422 AACAATGATGGAAGGCGTCGACGACTGTTTTGCCTATAAAATTCGATTTGATGGTGTGAA 481
                       ||||                 | ||       ||  |||||||
Db      333 CTCCCTGCAG――――――――――GACGGCTGCTTCATCTACAAGGTGAAGTTCATCGGCGTGAA 383

Qy      482 CTTTCCTGCCAATGGTCCAGTTATGCAGAGGAAGACGCTGAAAATGGGAGCCATCCACTGA 541
            ||||||||  |||| ||  |  ||||||| ||||||||  |||||||| |||||||||||
Db      384 CTTCCCCTCCGACGGGCCCCGTGATGCAGAGAAGACCATGGGCTGGGAGGCCTCCACCGA 443

Qy      542 GATAATGTATGCGCGTGATGGAGTGCTGAAGGGTGATGTTAACATGGCTCTTGTTGCTTGA 601
             ||  | ||||||||||  |  ||||||||||||||||| |||| || |  ||  || ||
Db      444 GCGGCCTGTACCCCGGACGGCGTGCTGAAGGGCGAGACCCACAAGGCCCTGAAGCTGAA 503

Qy      602 AGGAGGTGGGCCATTACCGATGTGACTTCAAAACTACTTACAAAGCTAAGAAGGTTGTCCG 661
            |  ||   | ||||    ||||    |||    |||  |||||| ||| || ||   |||
Db      504 GGACGGCGGCCACTACCTGGTGGAGTTCAAGTCCATCTACATGGCCAAGAGAGCCCCGTGCA 563

Qy      662 GTTGCCAGACTATCACTTTGTGGACCATGCGATTGAGATTGTGAGCCACCAGCAAAGATTA 721
            | |||| ||| |||| ||||  ||||||    || || ||||| ||||| |||| || ||
Db      564 GCTGCCCGGCTACTACTGGACGGCGCCAAGCTGGACATCACCTCCCACACGAGGAGACTA 623

Qy      722 CAACAAGGTTAAGCTGCACGAGCATGCCGAAGCTCGTCATGGACTGT 768
            ||| || ||| |  ||| | ||||   |||| | || |||||
Db      624 CACCATCGTGGAGCAGTACGAGCGCACCGAGGGCCGCCACCACCTGT 670
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Search completed: April 5, 2006, 21:43:39
Job time : 669 secs

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                Copyright   GenCore version 5.1.7
                            (c) 1993 - 2006   Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on:     April  5, 2006, 20:50:59 ; Search time 4977 Seconds
                              (without alignments)
                              10021.103 Million cell updates/sec

Title:      US-10-757-356-17
Perfect score:   1066
Sequence:   1 attcgccctggtgattgga.........atcgagccgaaaaaaaaa 1066

Scoring table::  IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters:          82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       EST:*
                 1: gb_est1:*
                 2: gb_est2:*
                 3: gb_est3:*
                 4: gb_htc:*
                 5: gb_est4:*
                 6: gb_est5:*
                 7: gb_est6:*
                 8: gb_est7:*
                 9: gb_gss1:*
                10: gb_gss2:*
                11: gb_gss3:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Match	Query Length	DB	ID	Description
	1	244.6	22.9	556	8	DR987866	DR987866 JGI_AOSF1
	2	241.4	22.6	556	8	DR987865	DR987865 JGI_AOSF1
	3	58	5.4	436	8	DR988183	DR988183 JGI_AOSF1
c	4	47.4	4.3	961	10	CL209197	CL209197 ZMBBb056
c	5	45.8	4.3	1201	10	CNS0107R	AL098625 Drosophil
c	6	45.4	4.2	1201	10	CNS01613	AL106161 Drosophil
c	7	44.4	4.2	319	8	DR986899	DR986899 JGI AOSC1
	8	44	4.1	678	8	DN886937	DN886937 naf40d08.
c	9	43.4	4.1	802	11	CNS0383B	AL232112 Tetraodon
c	10	43.2	4.1	895	9	CC154760	CC154760 CSU-K34.1
c	11	43.2	4.1	1101	10	CNS0039G	AL063921 Drosophil
c	12	42.8	4.0	443	2	BF588024	BF588024 FM1_35_G0
c	13	42.8	4.0	480	2	BF587508	BF587508 FM1_37_C0
c	14	42.8	4.0	517	2	BF587613	BF587613 FM1_38_F0
c	15	42.8	4.0	692	2	BF586807	BF586807 FM1_30_E1
c	16	42.4	4.0	395	1	AJ651923	AJ651923
c	17	42.4	4.0	397	1	AJ651934	AJ651934 AJ651923
c	18	42.4	4.0	482	1	AJ658699	AJ658699 AJ658699
c	19	42.4	4.0	660	5	BQ604452	BQ604452 MI-P-CP1-
c	20	42.4	4.0	707	6	CF789251	CF789251 866506 MA
c	21	42.2	4.0	772	10	CNS016XS	AL107338 Drosophil
c	22	42	3.9	737	5	BQ995633	BQ995633 QGG10I18.
c	23	41.6	3.9	1101	10	CNS016K3	AL106845 Drosophil
c	24	41.2	3.9	504	7	CV082013	CV082013 Mdfrt3069
c	25	41	3.8	725	10	AG183041	AG183041 Pan trogl
c	26	41	3.8	1101	10	CNS0021J	AL061936 Drosophil
c	27	41	3.8	1101	10	CNS00ESI	AL069797 Drosophil
c	28	40.6	3.8	1101	10	CNS016XR	AL107337 Drosophil
c	29	40.6	3.8	1188	10	AG305240	AG305240 Mus muscu
c	30	40.6	3.8	1366	9	CC228527	CC228527 CH261-157
c	31	40.4	3.8	1101	10	CNS0182P	AL108811 Drosophil
c	32	40.2	3.8	387	6	CA651996	CA651996 wrein.pk1
c	33	40.2	3.8	603	1	AW561384	AW561384 ga79d07.y
c	34	40.2	3.8	644	3	BJ591738	BJ591738
c	35	40.2	3.8	711	3	BJ579615	BJ579615
c	36	40.2	3.8	743	3	BJ167081	BJ167081
c	37	40.2	3.8	928	3	CNS0102F	AL098433 Drosophil
c	38	40	3.8	240	1	AV366735	AV366735
c	39	40	3.8	578	5	C91535	C91535 C91535 Dict
c	40	40	3.8	595	10	AG231618	AG231618 Lotus cor
c	41	40	3.8	668	3	BJ345340	BJ345340
c	42	40	3.8	706	3	BJ375096	BJ375096
c	43	39.8	3.7	647	3	BM499773	BM499773 95034G02
c	44	39.8	3.7	736	10	CL582087	CL582087 OB_Ba004
c	45	39.6	3.7	444	2	BI076362	BI076362 IP1_26_D0

ALIGNMENTS

```
RESULT 1
DR987866
LOCUS       DR987866                556 bp    mRNA        linear   EST 03-AUG-2005
DEFINITION  JGI_AOSF1131.fwd AOSF Montastraea faveolata adult colony
            Montastraea faveolata cDNA clone AOSF1131 5', mRNA sequence.
ACCESSION   DR987866
VERSION     DR987866.1  GI:7178257?
KEYWORDS    EST.
SOURCE      Montastraea faveolata
  ORGANISM  Montastraea faveolata
            Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Scleractinia;
            Faviina; Faviidae; Montastraea.
REFERENCE   1  (bases 1 to 556)
  AUTHORS   Schwarz,J.A., Brokstein,P., Manohar,C., Coffroth,M.A., Szmant,A.
            and Medina,M.
  TITLE     Coral-Symbiodinium EST Project
  JOURNAL   Unpublished (2005)
COMMENT     Other_ESTs: JGI AOSF1131.rev
            Contact: Schwarz, JA, Medina, M.
            Evolutionary Genomics
            DOE Joint Genome Institite
            2800 Mitchell Drive, Walnut Creek, CA 94598, USA
            Tel: 925-296-5823
            Email: jaschwarz@lbl.gov
            cDNA Library Preparation: DOE Joint Genome Institute:
            http://www.jgi.doe.gov
            DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov
            Naming Conventions: EST name is generated by the concatenation of
            the JGI Clone Id and the direction of sequencing. The suffix .fwd'
            indicates a forward sequencing read of the insert. It does not
            necessarily reflect the orientation of the insert.
            Small Insert: Based upon one or more sequencing reads of this clone
            where vector sequence was present at both ends, this clone has been
            determined to contain a cDNA insert on the order of 600-1000 bases.
            Plate: AOSF 0009 row: f column: 20
            High quality sequence stop: 557.
FEATURES             Location/Qualifiers
     source          1..556
                     /organism="Montastraea faveolata"
                     /mol_type="mRNA"
                     /db_xref="taxon:48498"
                     /clone="AOSF1131"
                     /dev_stage="Adult colony"
                     /lab_host="ElectroMAX DH10B"
                     /clone_lib="AOSF Montastraea·faveolata adult colony"
```

          /note="vector: pDNR-LIB; Site 1: SfiI; Site 2: SfiI; The
          library was prepared from total RNA using the Creator
          SMART cDNA Library Construction Kit with the LD-PCR method
          to amplify the cDNA. Amplified cDNA was digested with
          SfiI, size selected for >400bp, and ligated into the
          pDNR-LIB vector. WARNING: this library contains a small
          percentage of cDNAs derived from the coral's symbiont,
          Symbiodinium sp."

ORIGIN

Query Match   22.9%; Score 244.6; DB 8; Length 556;
Best Local Similarity   68.0%; Pred. No. 3.6e-58;
Matches 433; Conservative   0; Mismatches 114; Indels   90; Gaps   3;

Qy   183 GATGGAAAAGGAGGAAGCCTTCGACGGAACACAGAGACTATGGACCTTACAGTCATAGAGGC 242
         ||| |||| |||| |||||||||||||||| ||| ||||||||||| ||||||
Db   1 GACGGAGAAGGCAAGCCTTTCGAGGGAAAACACAGTATAAACCTTCAAGTCCAAGAAGGT 60

Qy   243 GCACCATTGCCTTCGCTTACGATATCTTGACAACAGTATTCGATTACGGCAACAGGGTA 302
         ||| ||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db   61 GGACCTCTCCCTTTGCTTACGATATCTTGACGACAGCATTCGTACGGCAACAGGGCA 120

Qy   303 TTCGCCAAATACCCAGAAGACATAGCAGATTATTTCAAGCAGACGTTCCTGAGGGGTAC 362
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 TTCACCAAATACCCAAGAGACCTCCCAGACTATTTCAAGCAGTCGTTCCTGCGGGGTAT 180

Qy   363 TTCTGGGAACGAAGCATGACATACGAGACCAGGGCATTTGCATCGCCACAAACGACATA 422
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TCCTGGGAACGTTGTATGACTTTCGAAGATGGAGGCATTTGCACCGTGTCAAACAACATC 240

Qy   423 ACAATGATGGAAGGCGTCGACGACTGTTTGCCTATAAAATTCGATTTGATGGTGTGAAC 482
         ||||
Db   241 AAAATG-------GAGGGCGACCGTTTTATCTATGATATTCGATTTCATGGTGTTAAC 291

Qy   483 TTTCCTGCCAATGGTCCAGTTATGCAGAGGAAGACGCTGAAATGGAGCCATCCACTGAG 542
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   292 TTTCCTGCTAATGGTCCAATTATGCAGAAGAGA----------------------- 325

Qy   543 ATAATGTATGCCGTGATGAGTGCTGAAGGGTGATGTTAACATGGTCTGTTGCTTGAA 602
                                                    ||||||||||||||||
Db   326 --CTCTGTTGCTTGAA 339

Qy   603 GGAGGTGGCCATTACCGATGTGACTTCAAAACTACTTACAAAGCTAAGAAGGTTGTCCGG 662
         ||| |||||||||||||||||||||| |||| |||||||||||||||||||
Db   340 GGAAATAAGCATCACCGATGTAACTTCAGAAGTACTTACAGAGGCCAAGAAGGATGTGGTG 399

Qy   663 TTGCCAGACTATCACTTTGTGACCATCGCATTGAGATTGTGAGCCACGACAAAGATTAC 722
         ||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db   400 TTGCCAGAATATCACTTTGTGACCACCGAATTGAGATATTAAGTCATGACAAAGATTAC 459

Qy   723 AACAAGGTTAAGCTGCACGAGCAGCGAAGGTCG--------TCATGGACTGTCAAGG 773
         ||||| |||||| ||||||||| |||||| ||| |||||| |||||
Db   460 AACAACGTGGTTGGTCTATGAGAATGCTGCTGCCCGCCCTCAGGCGTTCTACTCTCGCCGAGC 519

Qy   774 AAGGGCCCAAGTAAAGGCTTAATGAAAAGTCAAGACGAC 810
         ||||||||||||||||| |||| ||| |||||
Db   520 AAGGACAGTAAAGGCTTAACGAAGAGCCAAAAACGAC 556

RESULT 2
DR987865/c
LOCUS   DR987865   556 bp   mRNA   linear   EST 03-AUG-2005
DEFINITION JGI_AOSF1131.rev AOSF Montastraea faveolata adult colony
           Montastraea faveolata cDNA clone AOSF1131 3', mRNA sequence.
ACCESSION DR987865
VERSION   DR987865.1 GI:71782571
KEYWORDS   EST.
SOURCE   Montastraea faveolata
  ORGANISM Montastraea faveolata
           Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Scleractinia;
           Faviina; Faviidae; Montastraea.
REFERENCE 1 (bases 1 to 556)
  AUTHORS Schwarz,J.A., Brokstein,P., Manohar,C., Coffroth,M.A., Szmant,A.,

          and Medina,M.

FEATURES   Location/Qualifiers
     source   1..556
                 /organism="Montastraea faveolata"
                 /mol_type="mRNA"
                 /db_xref="taxon:48498"
                 /clone="AOSF1131"
                 /dev_stage="Adult colony"
                 /lab_host="ElectroMAX DH10B"
                 /clone_lib="AOSF Montastraea faveolata adult colony"
                 /note="Vector: pDNR-LIB; Site 1: SfiI; Site 2: SfiI; The
                 library was prepared from total RNA using the Creator
                 SMART cDNA Library Construction Kit with the LD-PCR method
                 to amplify the cDNA. Amplified cDNA was digested with
                 SfiI, size selected for >400bp, and ligated into the
                 pDNR-LIB vector. WARNING: this library contains a small
                 percentage of cDNAs derived from the coral's symbiont,
                 Symbiodinium sp."

ORIGIN

Query Match   22.6%; Score 241.4; DB 8; Length 556;
Best Local Similarity   67.7%; Pred. No. 3e-57;
Matches 431; Conservative   0; Mismatches 116; Indels   90; Gaps   3;

Qy   183 GATGGAAAAGGAGGAAGCCTTCGACGGAACACAGAGACTATGGACCTTACAGTCATAGAGGC 242
         ||| |||| |||| ||||||||||||||| ||| ||||||||||| ||||||
Db   556 GACGGAGAAGGCAAGCCTTTCGAGGGAAAACACAGTATAAACCTTCAAGTCCAAGAAGGT 497

Qy   243 GCACCATTGCCTTCGCTTACGATATCTTGACAACAGTATTCGATTACGGCAACAGGGTA 302
         ||| ||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db   496 GGACCTCTCCCTTTGCTTACGATATCTTGACGACAGCATTCGTACGGCAACAGGGCA 437

Qy   303 TTCGCCAAATACCCAGAAGACATAGCAGATTATTTCAAGCAGACGTTCCTGAGGGGTAC 362
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   436 TTCACCAAATACCCAAGAGACCTCCCAGACTATTTCAAGCAGTCGTTCCTGCGGGGTAT 377

Qy   363 TTCTGGGAACGAAGCATGACATACGAGACCAGGGCATTTGCATCGCCACAAACGACATA 422
         |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db   376 TCCTGGGAACGTTGTATGACTTTCGAAGATGGAGGCATTTGCACCGTGTCAAACAACATC 317

Qy   423 ACAATGATGGAAGGCGTCGACGACTGTTTGCCTATAAAATTCGATTTGATGGTGTGAAC 482
         ||||
Db   423 ACAATGATGGAAGGCGTCGACGACTGTTTGCC ... GATTTGATGGTGTGAAC 482

Qy   316 AAAATG------GAGGGCGACCGTTTTATCTATGATATTCGATTTCATGGTGTTAAC 266

Qy   483 TTTCCTGCCAATGGTCCAGTTATGCAGAGGAAGACGCTGAAATGGAGCCATCCACTGAG 542
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   265 TTTCCTGCTAATGGTCCAATTATGCAGAAGAGA---------------------- 232

Qy   543 ATAATGTATGCCGTGATGAGTGCTGAAGGGTCTGAAGGGTGATGTTAACATGGTCTGTTGCTTGAA 602
                                                     ||||||||||||||||

```
Query Match                 5.4%;    Score 58;   DB 8;   Length 436;
Best Local Similarity     65.0%;    Pred. No. 5.7e-05;
Matches 143; Conservative     0; Mismatches  55; Indels  22; Gaps  3;

Qy    765 CTGTCAAGGAAGGCCAAGTAAAGGCTTA-ATGAAAAGTCAAGACGACAACGAGAGAAGAAAC 823
          ||||||||||||||||||||||||||||| ||| || ||||||||||| || |||| |||
Db     32 CTGCCAAGCAAGGCAAAGTAAAGGCTTAGGGCAGAATAGTCAAGACGACAACAAGAAGAAAA  91

Qy    824 AAAGTACTTTTTGTTAAATTGAAGGCATTACTCCGGAATTAGTATTGATACTTTCGA 883
          |||||||  || |||| || |||||||||||||||||||||||| |||||||||||
Db     92 TAAAGTTGTTCAGATTAGAATTTGATATTCAGT-------------------TTTCGA 132

Qy    884 TTCAAGGATTGTTCCGGATTGTTAGAGACTAGCTTCGAGTTGTATTTTGTGAAAAA 943
          |||||||||||||||| |||||||||||||||||||||| ||||||||||
Db    133 TTCAAGGATTCGTTACGGGTTTGTTGTTAGAGACTAGCTTTAGAGT--TAAGTTTGCGAGAA 190

Qy    944 AGATAGTTTCCAGTTTTTGCGGATTACAGCATGGGGATA 983
          |||||| |||||||||||||||| |||||||||||||||
Db    191 AAAAGGTTTCCATTTTGCGCGCCGGTTTATAGCATAAGAGTA 230


RESULT 4
CL209197
CL209197/c
LOCUS        CL209197               961 bp    DNA       linear   GSS 07-JAN-2004
DEFINITION   ZMMBBb0562N23r ZMMBBb0562N23 (HindIII) Zea mays genomic clone
             ZMMBBb0562N23 3', genomic survey sequence.
ACCESSION    CL209197
VERSION      CL209197.1  GI:40725634
KEYWORDS     GSS.
SOURCE       Zea mays
  ORGANISM   Zea mays
             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
             Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
             clade; Panicoideae; Andropogoneae; Zea.
REFERENCE    1  (bases 1 to 961)
  AUTHORS    Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C.,
             Zohovetz,V., Fuks,G., Yu,Y., Wing,R. and Messing,J.
  TITLE      Sequencing of the maize genome at PGIR (2003c)
  JOURNAL    Unpublished (2003)
  COMMENT    Contact: Bharti,A.K.
             Dr.Joachim Messing's lab
             The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
             University
             190 Frelinghuysen Road, Piscataway, NJ 08854, USA
             Tel: 732 445 3801
             Fax: 732 445 5735
             Email: bharti@waksman.rutgers.edu
             Seq primer: SP6
             Class: BAC ends
             High quality sequence start: 101.
FEATURES             Location/Qualifiers
     source          1..961
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:4577"
                     /cultivar="B73"
                     /clone="ZMMBBb0562N23"
                     /lab_host="E. coli DH10B"
                     /clone_lib="ZMMBBb (HindIII)"
                     /note="Vector: pCUGI; Site_1: HindIII; Site_2: HindIII"
ORIGIN

Query Match                 4.4%;    Score 47.4;   DB 10;   Length 961;
Best Local Similarity     53.3%;    Pred. No. 0.077;
Matches 122; Conservative     0; Mismatches 106; Indels   1; Gaps  1;

Qy    815 AGGAGAAACAAAGTACTTTTTGTTAAATTGAAGGCATTTACTCCGGAATTAGTATTGA 874
          ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    599 ATGTCAATCTAAGAGAAGGATGTTCCTATTTTGAATTCATTTATTTATTTCTGATAAAATAGATGA 540

Qy    875 TACTTTCGATTCAAGGATTGTTCCGGGATTGTTGTTAGAGACTAGCTCTAGAGTTGTATT 934
          || ||||| ||||| ||||| ||| ||||||||| |||||||| |||||||||||||||
Db    539 TAATATTAAAATTTGATGGTTCAAGTTGGCTTTAGATTGAATATTGGCTTTGAATT 480
```

```
Qy      935  TGTGAAAAAAGTAGTTTCCAGTTTTTGCGGATTACAGCATGGGATAGAGACTTT--TAA  993
             ||||||   || ||||||  ||||||||||||||| || |||||||||||||  |||
Db      479  TAAGTAAATAGAAAGATTTTCATTTATTGGAGTGGATTATTTATATATATATATAT  420

Qy      994  ACTCAGTTGTGGTCAAATGCAAGTAAGAAAACTGTAGTGAGAATAAACT  1042
             ||||||| ||  ||||||||||||||| || | |||||||  |||||||
Db      419  AATTAGAAGTATTTATATACAAGAATGAAATGAAAACAATAAATAGAATGAAAT  371
```

RESULT 5
CNS0107R/c
LOCUS   CNS0107R   1201 bp   DNA   linear   GSS 26-JUL-1999
DEFINITION Drosophila melanogaster genome survey sequence T7 end of BAC
            BACN03G13 of DrosBAC library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL098625
VERSION   AL098625.1 GI:5610236
KEYWORDS   GSS.
SOURCE   Drosophila melanogaster (fruit fly)
  ORGANISM Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1 (bases 1 to 1201)
  AUTHORS   Genoscope.
  TITLE   Direct Submission
  JOURNAL   Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT   Determination of this BAC-end sequence was carried out as part of a
            collaboration with the European Drosophila Genome Project (EDGP) -
            http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
            library (Dros BAC) was made by Alain Billaud at CEPH (Centre
            d'Etude du Polymorphisme Humain) with funding provided by a MRC
            project grant. The DNA was prepared from embryos by Alain Bucheton
            and Genevieve Payan. It has been constructed in the vector
            pBeloBAC11.
FEATURES   Location/Qualifiers
     source   1..1201
                     /organism="Drosophila melanogaster"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7227"
                     /clone="BACN03G13"
                     /clone_lib="DrosBAC"
                     /plasmid="pBeloBAC11"
                     /note="end : T7"

ORIGIN
Query Match   4.3%; Score 45.8; DB 10; Length 1201;
Best Local Similarity 30.9%; Pred. No. 0.23;
Matches   77; Conservative 79; Mismatches 87; Indels   6; Gaps   1;

Qy   798 AAGTCAAGACGACCAACGAGGAGAAACAAAGTACTTTTTGTTAAATTGAAGGCATTAC 857
             :::::| |||: ::: || |: |||||||| ||::: | |||| |||| |:|::||
Db   798 WDDWTWARAGWGWRAVAARRGVGSAWRDDVAKTTTDVWDDTWTTTWKTWWAAWABAR 939

Qy   858 TCGGAATTAGTATTTGATACTTTCGATTCAAGGATTGTTCCCGGATTGTTAGAGACTA 917
             ||:|||||| :||:| ||| |: ::||||| ||| ||:| |||::: ||||||||
Db   938 WWWDATTTDTAWTTGATATTTTGATATTTWAKTRRDARDAADWKTTTTTGGDTTKAKTWTGRGWTW 879

Qy   918 ------GCTCTAGAGTTGTATTTTGTGAAAAAAGATAGTTTCCAGTTTTTGCGGGATTAC 971
             ::::: |:|: :| ||||||||||||||||||||||||||||||||||||||||||||
Db   878 ATGSGGRGRDMWTGGVKGGGDTDTVTRRSAGADWAWAWAWTTTGAWTAWTTTTARRTTTAA 819

Qy   972 AGCATGGGGATAGACTTTTAAACTCAGTTGTGTCAAATGCAAGTAAGAAAACTGTAGT 1031
             |:|||||| |:| :|| |: ||| : |:|:: || ||||||||||:|| |||::||
Db   818 ADTTTRRRAGWWGTDTDGKTKRGAGGWAGGDWAAATRGGAWRAAAKTAAATTATKBK 759

Qy   1032 GAGAATAAA 1040
             || ||:|
Db   758 KGAAAARRA 750
```

RESULT 6
CNS01613/c
LOCUS       CNS01613              1201 bp    DNA          linear   GSS 26-JUL-1999
DEFINITION  Drosophila melanogaster genome survey sequence SP6 end of BAC
            BACN15I08 of DrosBAC library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL106161
VERSION     AL106161.1  GI:5620457
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 1201)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the European Drosophila Genome Project (EDGP) -
            http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
            library (Dros BAC) was made by Alain Billaud at CEPH (Centre
            d'Etude du Polymorphisme Humain) with funding provided by a MRC
            project grant. The DNA was prepared from embryos by Alain Bucheton
            and Genevieve Payan. It has been constructed in the vector
            pBeloBAC11.
FEATURES             Location/Qualifiers
     source          1..1201
                     /organism="Drosophila melanogaster"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7227"
                     /clone="BACN15I08"
                     /clone_lib="DrosBAC"
                     /plasmid="pBeloBAC11"
                     /note="end : SP6"

ORIGIN
Query Match          4.3%;  Score 45.4;  DB 10;  Length 1201;
Best Local Similarity  39.3%;  Pred. No. 0.31;
Matches   68;  Conservative  35;  Mismatches  70;  Indels    0;  Gaps    0;

Qy      780  AAGTAAAGGCTTAATGAATGAAAGTCAAGACGACAACGAGGAGAAACAAAGTACTTTTTGT  839
             || ||| ||||:||| ||| |||||| | ||  || | ||||||||||||||| :|::||
Db     1162  AAWTDGGGAAAAAAATAATGTRAAAAATTGAAAAAAATWGAAAWAAAAWTTKT  1103

Qy      840  AAATTTGAAGGCATTTACTCGGAATTAGTATTTGATACTTTCGATTCAAGGATTTGTTCC  899
             :||||||| :|:| |||  |:|| || :|| | ||||:|||| :| ||  ::|| |:|:|
Db     1102  WAATKTGAAWWAWWTWDTTWDAAWAKATAATTWTWTWTTTAAWWTKATGGKKKTKTTKK  1043

Qy      900  GGGATTTGTTGTAGAGACTAGCTCTAGAGTTGTATTTTGTGAAAAAAGATAGTTT  952
             ||||||  | |  :|| :|::| ::: :| ||||||||||||||||||||||||:
Db     1042  TTTTTKTTTTKTTRKGKKTTKTTMAATTTTTKTTTGKKDAWWAAAAWWAGGKT  990

RESULT 7
DR986899
LOCUS       DR986899               319 bp    mRNA         linear   EST 03-AUG-2005
DEFINITION  JGI_AOSC1075.fwd AOSC Montastraea faveolata 60 hours post
            fertilization Montastraea faveolata cDNA clone AOSC1075 5', mRNA
            sequence.
ACCESSION   DR986899
VERSION     DR986899.1  GI:71781605
KEYWORDS    EST.
SOURCE      Montastraea faveolata
  ORGANISM  Montastraea faveolata
            Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Scleractinia;
            Faviina; Faviidae; Montastraea.
REFERENCE   1  (bases 1 to 319)
  AUTHORS   Schwarz,J.A., Brokstein,P., Manohar,C., Coffroth,M.A., Szmant,A.
            and Medina,M.
```

TITLE   Coral-Symbiodinium EST Project
JOURNAL   Unpublished (2005)
COMMENT   Other ESTs: JGI_AOSC1075.rev
Contact: Schwarz, JA, Medina, M.
Evolutionary Genomics
DOE Joint Genome Institite
2800 Mitchell Drive, Walnut Creek, CA 94598, USA
Tel: 925-296-5823
Email: jaschwarz@lbl.gov
cDNA Library Preparation: DOE Joint Genome Institute:
http://www.jgi.doe.gov/
DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov
Naming Conventions: EST name is generated by the concatenation of
the JGI Clone Id and the direction of sequencing. The suffix '.fwd'
indicates a forward sequencing read of the insert. It does not
necessarily reflect the orientation of the insert.
Small insert: Based upon one or more sequencing reads of this clone
where vector sequence was present at both ends, this clone has been
determined to contain a cDNA insert on the order of 600-1000 bases.
Plate: AOSC 0009 row: f column: 6
High quality sequence stop: 319.

FEATURES   Location/Qualifiers
source   1..319
/organism="Montastraea faveolata"
/mol_type="mRNA"
/db_xref="taxon:48498"
/clone="AOSC1075"
/dev_stage="60 hour post fertilization"
/lab_host="ElectroMAX DH10B"
/clone_lib="AOSC Montastraea faveolata 60 hours post
fertilization"
/note="Vector: pDNR-LIB; Site_1: SfiI; Site 2: SfiI; The
library was prepared from total RNA using the Creator
SMART cDNA Library Construction Kit with the LD-PCR method
to amplify the cDNA. Amplified cDNA was digested with
SfiI, size selected for >400bp, and ligated into the
pDNR-LIB vector."

ORIGIN

Query Match 4.2%; Score 44.4; DB 8; Length 319;
Best Local Similarity 50.0%; Pred. No. 0.39;
Matches 108; Conservative 0; Mismatches 108; Indels 0; Gaps 0;

```
Qy  851 CATTTACTCGGAATTAGTATTGATACTTTCGATTCAAGGATTTGTTCCGGGATTTGTTA 910
            ||||| ||||| ||||| ||  |||||| |||| ||| ||| |||||  |||
Db   91 CAGAGACTAGGAAGGAGAACTTGATCATTTGATCATTCGATAAAGTAAATGTATAATTT 150

Qy  911 GAGACTAGCTCTAGAGTTGTATTTGTGAAAAAAGATAGTTCCAGTTTTGCGGGATTA 970
            || ||||| |||| |||| |  ||| ||||||   |||||
Db  151 GAAACAAACTGCAGAGTCCGTTACTCGGCGCATTTAGTTTGATGTTTATCATATAAAT 210

Qy  971 CAGCATGGGGATAGACTTTTTAAACTCAGTTGTGTCAAATGCAAGTAAGAAAACTGTAG 1030
            |||| |  || ||| ||||||
Db  211 TACTGGCGGTTGATTCACTTCACTTAATTGCGTTCACTAGTTCAAATAAATGTGGAA 270

Qy 1031 TGAGAATAAACTTGTTATCGAAGCCGAAAAAAAAA 1066
            ||||||| || ||||||||||||||
Db  271 TTAAAATGATTTCTTGCNNAAAAAAAAAAAAAAAA 306
```

RESULT 8
DN886937
LOCUS   DN886937   678 bp   mRNA   linear   EST 21-APR-2005
DEFINITION   naf40008.x1 Rabbit eye cornea. Unnormalized (naf) Oryctolagus
cuniculus cDNA clone naf40008 3', mRNA sequence.
ACCESSION   DN886937
VERSION   DN886937.1   GI:62856892
KEYWORDS   EST.
SOURCE   Oryctolagus cuniculus (rabbit)
ORGANISM   Oryctolagus cuniculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha;
Leporidae; Oryctolagus.

REFERENCE   1 (bases 1 to 678)
AUTHORS   Wistow,G.
TITLE   NEIBank analysis of Rabbit cornea
JOURNAL   Unpublished (2005)
COMMENT   Contact: Wistow G
Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
Email: graeme@helix.nih.gov
Plate: 40 row:d column: 08
Seq primer: Universal -21M13 Forward.

FEATURES   Location/Qualifiers
source   1..678
/organism="Oryctolagus cuniculus"
/mol_type="mRNA"
/db_xref="taxon:9986"
/clone="naf40008"
/tissue_type="cornea"
/dev_stage="Adult"
/lab_host="EMDH10B"
/clone_lib="Rabbit eye cornea. Unnormalized (naf)"
/note="Organ: Eye; Vector: pCMVSport6; RNA was extracted
from Rabbit cornea tissue. A directionally cloned cDNA
library in the pCMVSPORT6 vector (Invitrogen) was
constructed at Bioserve Biotechnology (Laurel MD)
essentially following the protocols of the SuperScript
Plasmid System, full details of which are contained in the
manufacturer's Instruction manual
(http://www.lifetech.com/). First strand synthesis was
carried out using a Not I primer-adapter
[5'-pGACTAGTTCTAGATCGGCGAGCGGCGCCC(T)15-3']. cDNA was
cloned in Not I/Sal I sites. EST analysis was performed at
the NIH Intramural Sequencing Center (NISC). Analyzed data
available through http://neibank.nei.nih.gov."

ORIGIN

Query Match 4.1%; Score 44; DB 8; Length 678;
Best Local Similarity 49.2%; Pred. No. 0.64;
Matches 116; Conservative 0; Mismatches 120; Indels 0; Gaps 0;

```
Qy  831 TTTTTGTTAAATTGAAGGCATTACTCGGAATTAGTATTGATACTTTCGATTCAAGG 890
            ||||| |||||| ||||||| ||| ||| |||| ||||
Db   13 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 72

Qy  891 ATTTGTTCCGGGATTTGTTAGAGACTAGCTCTAGAGTTGTATTTGTGAAAAAAGATAGT 950
            |||| ||
Db   73 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAAAAAAAATTTT 132

Qy  951 TTCCAGTTTTGCGGGATTACAGCATGGGGATAGACTTTTTAAACTCAGTTGTGTCAAA 1010
            ||||||
Db  133 TTTTTTTTTTTTTTTTTTTAAAAAAAAATGGGGATAAAAAAATTTTTATTATTTTTTTTTT 192

Qy 1011 TGCAGTAAGAAAACTGTAGTGAGAATAAACTTGTTATCGAAGCCGAAAAAAAAA 1066
            ||| ||||
Db  193 TTAAAAAAAAAAGGGGGGAAAAAAAAAAAAAACCCCCAAAACCAAAAAAAAAA 248
```

RESULT 9
CNS0383B/c
LOCUS   CNS0383B   802 bp   DNA   linear   GSS 01-SEP-2000
DEFINITION   Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
004012 of library G from Tetraodon nigroviridis, genomic survey
sequence.
ACCESSION   AL232112
VERSION   AL232112.1   GI:7891247
KEYWORDS   GSS; genome survey sequence.
SOURCE   Tetraodon nigroviridis
ORGANISM   Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

REFERENCE   1
AUTHORS   Tetradontoidea; Tetraodontidae; Tetraodon.
            Roest Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
TITLE   Estimate of human gene number provided by genome-wide analysis
            using Tetraodon nigroviridis DNA sequence
JOURNAL   Nat. Genet. 25 (2), 235-238 (2000)
PUBMED   10835645
REFERENCE   2
AUTHORS   Roest Crollius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,
            Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
            Saurin,W., Bernot,A. and Weissenbach,J.
TITLE   Characterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetraodon nigroviridis
JOURNAL   Genome Res. 10 (7), 939-949 (2000)
PUBMED   10899143
REFERENCE   3   (bases 1 to 802)
AUTHORS   Genoscope.
TITLE   Direct Submission
JOURNAL   Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT   This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/Tetraodon.
FEATURES   Location/Qualifiers
     source   1..802
                     /organism="Tetraodon nigroviridis"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:99883"
                     /clone="004O12"
                     /clone_lib="G"
                     /note="Genoscope sequence ID : COBG004BH06XE1
                     end : PUC-Ori"
ORIGIN

Query Match   4.1%; Score 43.4; DB 11; Length 802;
Best Local Similarity 41.9%; Pred. No. 1;
Matches 101; Conservative 22; Mismatches 118; Indels 0; Gaps 0;

Qy   825 AGTACTTTTTTGTTAAATTTGAAGGCATTTACTCGGAATTAGTATTTGATACTTTCGAT 884
              |:|| ||||| | ||| :: :|| ||| | || :||| || ||
Db   320 AWKTTTTATTTTTWTTTAATTTATGTKGWKTGAAKTWATARAAAAATAWRAGATTTTAT 261

Qy   885 TCAAGGATTGGTCCGGGATTGTTAGAGACTAGCTCCTAGAGTTGTATTTGTGAAAAAA 944
              | |||| |||||||||||| | | | ||| || |:|||||||||||||||
Db   260 TAAAGTKTAKTTTTTTTKTTTTTATAAAATTTTAAGKAKTTTWTAAGKTTTAATA 201

Qy   945 GATAGTTTCCAGTTTTGCGGGATTACAGCATGGGGATAGACTTTTTAAACTCAGTTGTG 1004
              |||||| |: ||| ||||||: :| |||| :| | :||| | |:||
Db   200 AATTTTKTTTTGKTTGGAGAGTGTGTTAGTGGGGGGTGAATGTGTAGGGTRARATGTG 141

Qy   1005 GTCAAATGCAAGTAAGAGAAAACTGTAGTGAGAATAAACTGTTATCGAAGCCGAAAAAAA 1064
              : |||| ::| |||||| ||| |: || |
Db   140 RAGAAAARARAGGGGAAAAAAGAGAAGAGRAGGTTKTRTTTAAAAGRGGTTAATRAT 81

Qy   1065 A 1065
              |
Db   80 A 80

RESULT 10
CC154760/c
LOCUS   CC154760   895 bp   DNA   linear   GSS 25-APR-2003
DEFINITION CSU-K34.122B16.SP6 CSU-K34 Aedes aegypti genomic clone
            CSU-K34-122B16, genomic survey sequence.
ACCESSION   CC154760
VERSION   CC154760.1 GI:30108056
KEYWORDS   GSS.
SOURCE   Aedes aegypti (yellow fever mosquito)
ORGANISM   Aedes aegypti

            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
            Culicidae; Culicinae; Culicini; Aedes; Stegomyia.
REFERENCE   1   (bases 1 to 895)
AUTHORS   Loftus,B., Shetty,J., Knudson,D. and Severson,D.
TITLE   BAC end sequencing of Aedes aegypti
JOURNAL   Unpublished (2003)
COMMENT   Other_GSSs: CSU-K34.122B16.T7
            Contact: Brendan Loftus
            Department of Eukaryotic Genomics
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301-838-3543
            Fax: 301-838-0208
            Email: enta@tigr.org
            Library was provided by Susan Brown and Dennis Knudson at Colorado
            State University.
            Seq primer: SP6
            Class: BAC ends.
FEATURES   Location/Qualifiers
     source   1..895
                     /organism="Aedes aegypti"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7159"
                     /clone="CSU-K34-122B16"
                     /clone_lib="CSU-K34"
                     /note=Vector: pBACe3.6; Site_1; EcoRI; Source DNA: Aedes
                     aegypti; strain unknown (derived from freshly hatched
                     larvae at the Virus Research Centre, Poona, India.
                     Reference: SINGH, K. R. P., 1967 Cell cultures derived
                     from larvae of Aedes albopictus (Skuse) and Aedes aegypti
                     (L.). Current Science 36: 506-508]; ATC-10 cell line ATCC
                     CCL-125"
ORIGIN

Query Match   4.1%; Score 43.2; DB 9; Length 895;
Best Local Similarity 48.4%; Pred. No. 1.2;
Matches 120; Conservative 0; Mismatches 128; Indels 0; Gaps 0;

Qy   818 AGAAACAAAGTACTTTTTTGTTAAATTTGAAGCATTTACTCGGAATTAGTATTTGATAC 877
              |||| |||| ||| ||||||||||||||||||| ||||||
Db   367 ATAATTAAATTATAAATGTTTGCATTCATTCGAAAAAGTTCTAAATTAGTCATGATTGT 308

Qy   878 TTTCGATTCAAGGATTGTTCCGGGATTTGTTAGAGACTAGCTCTACAGTTGTATTTTGT 937
              ||||||| | ||||| ||||| ::||| |||||||||||
Db   307 TACAAAATTTCGAATTTAAAGTTGTTCAAATTCCAGTTTACCTTTCCGATTTTTTTTTCT 248

Qy   938 GAAAAAAGATAGTTCCAGTTTTGCGGGATTACAGCATGCGGGATAGACTTTTTAAACTC 997
              ||||||| ||| |||||||||||||||||| | |||| :|||||
Db   247 GGAATTAAAATATTTTCCAATAATTTTGAAATTGTGCATGAGAGGCTTTCACCATCATGAG 188

Qy   998 AGTTGTGTCAAATGCAAGTGAGTAAGAAAACTGTAGTGAGAATAAACTGTTATCGAAGCCGA 1057
              |||| |: | |||| :||| || :|||| ||| |||| |||| :|||
Db   187 TTTCTTGAAAATACGAAATTTAGAAACCTCTTTCCAGAAAAAAAGTGATTAAAAAGAAAC 128

Qy   1058 AAAAAAAA 1065
              |||||||
Db   127 CAAAAAAA 120

RESULT 11
CNS0039G/c
LOCUS   CNS0039G   1101 bp   DNA   linear   GSS 03-JUN-1999
DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC #
            BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL063921
VERSION   AL063921.1 GI:4941778
KEYWORDS   GSS.
SOURCE   Drosophila melanogaster (fruit fly)
ORGANISM   Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

```
REFERENCE      Ephydroidea; Drosophilidae; Drosophila.
AUTHORS        Genoscope.
TITLE          Direct Submission
JOURNAL        Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
               BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
               - Web : www.genoscope.cns.fr)
COMMENT        Determination of this BAC-end sequence was carried out as part of a
               collaboration with the Berkeley Drosophila Genome Project (BDGP).
               The BDGP is constructing a physical map of the Drosophila
               melanogaster genome using these BACs. For further information
               please see http://www.fruitfly.org The BDGP Drosophila
               melanogaster BAC library was prepared by Kazutoyo Osoegawa and
               Aaron Mammoser in Pieter de Jong's laboratory in the Department of
               Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
               NY. The library is named RPCI-98 and was constructed by partial
               EcoRI digestion of Drosophila DNA provided by the BDGP from the
               isogenic strain y2; cn bw sp. the same strain used for the BDGP's
               P1 and EST libraries. A more detailed description of the library
               and how to order individual BAC clones, the entire library, or
               filters for hybridization from the BACPAC Resource Center can be
               found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES       Location/Qualifiers
     source    1..1101
               /organism="Drosophila melanogaster"
               /mol_type="genomic DNA"
               /db_xref="taxon:7227"
               /clone="BACR08K10"
               /clone_lib="RPCI-98"
               /note="end : TET3"
ORIGIN

Query Match       4.1%;  Score 43.2;  DB 10;  Length 1101;
Best Local Similarity  13.8%;  Pred. No. 1.3;
Matches  75;  Conservative 249;  Mismatches 216;  Indels 2;  Gaps 1;

Qy    420 ATAACAATGATGGAAGGCGTCGACGACTGTTTGCCTATAAAATTCGATTTGATGGTGTG 479
              : : |::::|: ||:: ||:: : : ::| :|| ::|:| ::::||
Db   1074 WWKDRADDRRWAGDADRWAWDDGAGTWWTATWWWWWWWATWDTWWDKWWWWATAAKTDT 1015

Qy    480 AACTTTCCTGCCAATGGTCCAGTTATGCAGAGGAAGACGCCTGAAATGGGAGCCATCCACT 539
              : |:||: ||| : :|:| |:||:|
Db   1014 AWTWWRTAWRADWAGRDRGAGKRDRDAATDADGAGRRDGGRKRDKDRKDGDDDKKGGK 955

Qy    540 GAGATAAATGTATGCGCGTGATGGAGTGCTGAAGGGTGATGTTAACATGGCTCTGTTGCTT 599
              : :| | :|| ::::::::: ::: ::|::: : |:| |:::: :|::::::
Db    954 KKKAAKAAKWATKWWDWDWDKDWKDWGKADKRKADDDDGAGKDDDGKGKDADDDTDGTK 895

Qy    600 GAAGGAGGTGGCCATTACCCATGGTGACTTCAAAACTACTTACAAAGCTAAGAAGGTTGTC 659
              :::::: : ::|| ||| ::::: ::|:|::: |:::::|:
Db    894 DDDDKDKWDDWDKAKGTWGDATWAWAATDWWWWGWADADWWTWDAAADDWWADDRWDAWA 835

Qy    660 CGGTTGCCAGACTATCACTTTGTGGACCATCGCCATTGAGATTGTGAGCCACGACAAAGAT 719
              ||| :| |:: : : ::| ::|:: ::| |:::: :|:
Db    834 WKWDDAWAWGARTADRRDWGDRAGKRGGA--RKGRDRKRADDKRDAADRDDAATWTTWT 777

Qy    720 TACAACAAGGTTAAGCTGCACGAGCATGCCAAGCTCGTCATGGACTGTCAAGGAAGGCC 779
              | :: : ::: ::: : :|| |: ::: :|:: |:::|: |:|
Db    776 TTTTRDTDDWKWKTDTWTRWAADRTWDRDDDDRDRAGTAGRKWRRTWKRRWKRRDTRWD 717

Qy    780 AAGTAAAGGCTTAATGAAAAGTCAAGACGAGAAACAAGTACTTTTTTGTT 839
              :|: ::: | :: |: :|:: :|:: |: ::: ||:::::
Db    716 DADADDTARDDRRRRRGDDGADAGKGKKTGRKRRRRRDRAATWDRTDAWWADAAWWTTTDTDT 657

Qy    840 AAATTTGAAGGCATTTACTCGGAATTAGTATTTGATACTTTCGATTCAAGGATTTGTTCC 899
              :::: :::::: :||:||:: |::|: ::::|| | ::|:
Db    656 DDWDKDRDRRKGARRRRRTTARAAWDWWTWKAWDWAKWDWKTRADRWDRWAADTWTDARK 597

Qy    900 GGGATTTGTTAGAGACTAGCTCTAGAGTTGTATTTTGTGAAAAAAAGATAGTTTCCAGTTT 959
              :::: :: :::| : ::|:|: :: |: |: :|||: ::::||
Db    596 ADRDWAKARAWRARRDRARAAARADRRWTTKGKTTTATWTTWAARAAWWAWWATTTATW 537

Qy    960 TT 961
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```
Db   536 TT 535

RESULT 12
BF588024/c
LOCUS          BF588024                  443 bp    mRNA    linear    EST 12-DEC-2000
DEFINITION     FM1_35_G05.g1_A003 Floral-Induced Meristem 1 (FM1) Sorghum
               propinquum cDNA, mRNA sequence.
ACCESSION      BF588024
VERSION        BF588024.1  GI:11680348
KEYWORDS       EST.
SOURCE         Sorghum propinquum
ORGANISM       Sorghum propinquum
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
               clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE      1  (bases 1 to 443)
AUTHORS        Cordonnier-Pratt,M.-M., Gingle,A., Sudman,M., Marsala,C. and
               Pratt,L.H.
TITLE          An EST database from Sorghum: floral-induced meristems
JOURNAL        Unpublished (2000)
COMMENT        Contact: Cordonnier-Pratt MM
               Laboratory for Genomics and Bioinformatics
               The University of Georgia, Department of Plant Biology
               Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
               Tel: 706 542 1860
               Fax: 706 583 0210
               Email: mmpratt@uga.edu
               Sequences have been trimmed to exclude PolyA, vector and regions
               below Phred quality 16. The threshold for highest quality sequence
               is 20.
               Seq primer: PolyTMix
               High quality sequence start: 36
               High quality sequence stop: 429
               POLYA=Yes.
FEATURES       Location/Qualifiers
     source    1..443
               /organism="Sorghum propinquum"
               /mol_type="mRNA"
               /db_xref="taxon:132711"
               /clone_lib="Floral-Induced Meristem 1 (FM1)"
               /note="Organ: Floral-induced meristems; Vector:
               pBluescript II from Lambda Zap II; Site 1: XhoI; Site 2:
               EcoRI; mature plants were placed in a growth chamber for
               15 days with 16 hr darkness and 8 hr light (flowering is
               induced by short-day conditions); 16 days after being
               returned to the greenhouse under natural long days during
               late April/early May, meristems were harvested The
               library was made from poly-A RNA in the cloning vector
               lambda ZAP II. Clones to be sequenced were prepared by
               mass excision."
ORIGIN

Query Match       4.0%;  Score 42.8;  DB 2;  Length 443;
Best Local Similarity  54.4%;  Pred. No. 1.2;
Matches  86;  Conservative  0;  Mismatches 72;  Indels 0;  Gaps 0;

Qy     55 TTGATATCTTACTTACGTCTACCATCATGACAAGTGTTGCACAGGAAAAGGGTGTGATTA 114
           ||||||  |||||||| ||| |||||  ||||   |||   | |||||
Db    288 TAGATAACCTAGTACCCTATGCTTTGGTACGTACGGAAGTGCTGTCCAGTACTCGTGAAGAGGGTGCTTA 229

Qy    115 AACCAGACATGAAGATGAAGCTGCCTATGGAAGGTGCTGTAAACGGGCACAAGTTCGTGG 174
           ||||| :: |:: :|| :|: |:| |:| ||| :|::::|| |::
Db    228 GGTCAGTCGATCACAGTTCACAGCTCCGGCTGGGGTCTATAGGCTGCCTCCTTCAGGAAGTTA 169

Qy    175 TTGAAGGAGATGGAAAAGGGAAGCCTTTGCACGGAACA 212
           |||||| | | ||  :|:| |||| :| ||| ||||
Db    168 TCGAAGGGGCTGGCAGGTGGAGTTTACTACAGAACA 131

RESULT 13
BF587508/c
```

LOCUS   BF587508   480 bp   mRNA   linear   EST 12-DEC-2000
DEFINITION FM1_37_C08.g1_A003 Floral-Induced Meristem 1 (FM1) Sorghum
            propinquum cDNA, mRNA sequence.
ACCESSION   BF587508
VERSION   BF587508.1 GI:11679832
KEYWORDS   EST.
SOURCE   Sorghum propinquum
  ORGANISM Sorghum propinquum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE   1 (bases 1 to 480)
  AUTHORS   Cordonnier-Pratt,M.-M., Gingle,A., Sudman,M., Marsala,C. and
            Pratt,L.H.
  TITLE   An EST database from Sorghum: floral-induced meristems
  JOURNAL   Unpublished (2000)
COMMENT   Contact: Cordonnier-Pratt MM
            Laboratory for Genomics and Bioinformatics
            The University of Georgia, Department of Plant Biology
            Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
            Tel: 706 542 1860
            Fax: 706 583 0210
            Email: mmpratt@uga.edu
            Sequences have been trimmed to exclude PolyA, vector and regions
            below Phred quality 16. The threshold for highest quality sequence
            is 20.
            Seq primer: PolyTMix
            High quality sequence start: 5
            High quality sequence stop: 477
            POLYA=No.
FEATURES   Location/Qualifiers
     source   1..480
                     /organism="Sorghum propinquum"
                     /mol_type="mRNA"
                     /db_xref="taxon:132711"
                     /clone_lib="Floral-induced Meristem 1 (FM1)"
                     /note="Organ: Floral-induced meristems; Vector:
                     pBluescript II from Lambda Zap II; Site 1: XhoI; Site 2:
                     EcoRI; mature plants were placed in a growth chamber for
                     15 days with 16 hr darkness and 8 hr light (flowering is
                     induced by short-day conditions); 16 days after being
                     returned to the greenhouse under natural long days during
                     late April/early May, meristems were harvested The
                     library was made from poly-A RNA in the cloning vector
                     lambda ZAP II. Clones to be sequenced were prepared by
                     mass excision."
ORIGIN

Query Match   4.0%;   Score 42.8;   DB 2;   Length 480;
Best Local Similarity   54.4%;   Pred. No. 1.3;
Matches   86;   Conservative   0;   Mismatches   72;   Indels   0;   Gaps   0;

Qy   55 TTGATATCTTACTTACGTCTCACCATCATGACAAGTGTTGCACAGGAAAAGGGTGTGATTA 114
          |||| | |||| |||| | || ||| || || |||||||||||| |||||||| || ||
Db   294 TAGATAACCTAGTACCCTATGCTTTGGTACGCAGTCTAGCACGTGCTGCTTA 235

Qy   115 AACCAGACATGAAGATGAAGCTGCGTATGGAAGCTGGCGTGTAAACGGGCCACAAGTTCGTGG 174
          |||| | ||| |||| |||| || || |||||||| | ||||||||||| ||||||||||
Db   234 GGTCAGTCGATCACAGTTCACAGCTCCGGCTGGGTGGTGCTATAGGCCTTCAGGAAGTTA 175

Qy   175 TTGAAGGAGATGGAAAAGGGAAGCCTTTCGACGGAACA 212
          | ||||| | ||| | |||||||| || |||| |||
Db   174 TCGAAGGGGGCTGGCAGGTGGAAGCTTTACTACAGAACA 137

RESULT 14
BF587613/c
LOCUS   BF587613   517 bp   mRNA   linear   EST 12-DEC-2000
DEFINITION FM1_38_F03.g1_A003 Floral-Induced Meristem 1 (FM1) Sorghum
            propinquum cDNA, mRNA sequence.
ACCESSION   BF587613
VERSION   BF587613.1 GI:11679937
KEYWORDS   EST.

SOURCE   Sorghum propinquum
  ORGANISM Sorghum propinquum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE   1 (bases 1 to 517)
  AUTHORS   Cordonnier-Pratt,M.-M., Gingle,A., Sudman,M., Marsala,C. and
            Pratt,L.H.
  TITLE   An EST database from Sorghum: floral-induced meristems
  JOURNAL   Unpublished (2000)
COMMENT   Contact: Cordonnier-Pratt MM
            Laboratory for Genomics and Bioinformatics
            The University of Georgia, Department of Plant Biology
            Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
            Tel: 706 542 1860
            Fax: 706 583 0210
            Email: mmpratt@uga.edu
            Sequences have been trimmed to exclude PolyA, vector and regions
            below Phred quality 16. The threshold for highest quality sequence
            is 20.
            Seq primer: PolyTMix
            High quality sequence start: 132
            High quality sequence stop: 511
            POLYA=No.
FEATURES   Location/Qualifiers
     source   1..517
                     /organism="Sorghum propinquum"
                     /mol_type="mRNA"
                     /db_xref="taxon:132711"
                     /clone_lib="Floral-Induced Meristem 1 (FM1)"
                     /note="Organ: Floral-induced meristems; Vector:
                     pBluescript II from Lambda Zap II; Site 1: XhoI; Site 2:
                     EcoRI; mature plants were placed in a growth chamber for
                     15 days with 16 hr darkness and 8 hr light (flowering is
                     induced by short-day conditions); 16 days after being
                     returned to the greenhouse under natural long days during
                     late April/early May, meristems were harvested The
                     library was made from poly-A RNA in the cloning vector
                     lambda ZAP II. Clones to be sequenced were prepared by
                     mass excision."
ORIGIN

Query Match   4.0%;   Score 42.8;   DB 2;   Length 517;
Best Local Similarity   54.4%;   Pred. No. 1.3;
Matches   86;   Conservative   0;   Mismatches   72;   Indels   0;   Gaps   0;

Qy   55 TTGATATCTTACTTACGTCTCACCATCATGACAAGTGTTGCACAGGAAAAGGGTGTGATTA 114
          |||| | |||| |||| | || ||| || || |||||||||||| |||||||| || ||
Db   396 TAGATAACCTAGTACCCTATGCTTTGGTACGCAGTCTAGCACGTGCTGCTTA 337

Qy   115 AACCAGACATGAAGATGAAGCTGCGTATGGAAGCTGGCGTGTAAACGGGCACAAGTTCGTGG 174
          |||| | ||| |||| |||| || || |||||||| | ||||||||||| |||||||||
Db   336 GGTCAGTCGATCACAGTTCACAGCTCCGGCTGGGTGGTGCTATAGGCCTTCAGGAAGTTA 277

Qy   175 TTGAAGGAGATGGAAAAGGGAAGCCTTTCGACGGAACA 212
          | ||||| | ||| | |||||||| || |||| |||
Db   276 TCGAAGGGGGCTGGCAGGTGGAAGCTTTACTACAGAACA 239

RESULT 15
BF586807/c
LOCUS   BF586807   692 bp   mRNA   linear   EST 12-DEC-2000
DEFINITION FM1_30_E11.g1_A003 Floral-Induced Meristem 1 (FM1) Sorghum
            propinquum cDNA, mRNA sequence.
ACCESSION   BF586807
VERSION   BF586807.1 GI:11679033
KEYWORDS   EST.
SOURCE   Sorghum propinquum
  ORGANISM Sorghum propinquum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE   1 (bases 1 to 692)

AUTHORS   Cordonnier-Pratt,M.-M., Gingle,A., Sudman,M., Marsala,C. and
            Pratt,L.H.
TITLE   An EST database from Sorghum: floral-induced meristems
JOURNAL   Unpublished (2000)
COMMENT   Contact: Cordonnier-Pratt MM
            Laboratory for Genomics and Bioinformatics
            The University of Georgia, Department of Plant Biology
            Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
            Tel: 706 542 1860
            Fax: 706 583 0210
            Email: mmpratt@uga.edu
            Sequences have been trimmed to exclude PolyA, vector and regions
            below Phred quality 16. The threshold for highest quality sequence
            is 20.
            Seq primer: PolyTMix
            High quality sequence start: 62
            High quality sequence stop: 691
            POLYA=No.
FEATURES   Location/Qualifiers
     source   1..692
                /organism="Sorghum propinquum"
                /mol_type="mRNA"
                /db_xref="taxon:132711"
                /clone_lib="Floral-induced Meristem 1 (FM1)"
                /note="Organ: Floral-induced meristems; Vector:
                pBluescript II from Lambda Zap II; Site_1: XhoI; Site_2:
                EcoRI; mature plants were placed in a growth chamber for
                15 days with 16 hr darkness and 8 hr light (flowering is
                induced by short-day conditions); 16 days after being
                returned to the greenhouse under natural long days during
                late April/early May, meristems were harvested The
                library was made from poly-A RNA in the cloning vector
                lambda ZAP II. Clones to be sequenced were prepared by
                mass excision."

ORIGIN

Query Match   4.0%;   Score 42.8; DB 2;   Length 692;
Best Local Similarity   54.4%;   Pred. No. 1.4;
Matches   86; Conservative   0; Mismatches   72; Indels   0; Gaps   0;

Qy   55 TTGATATCTTACTTACGTCTACCATCATGACAAGTGTTGCACAGGAAAAGGGTGTGATTA 114
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Db   536 TAGATAACCTAGTACCCTATGCTTTGTACCGCAGTCTAGCACTCGTGAAGAGGGTGCTTA 477

Qy   115 AACCAGACATGAAGATGAAGCTGCGTATGGAAGGTGCTGTAAACGGGCACAAGTTCGTGG 174
          ||| ||| || ||| || ||||||||| |||||||| || |||||||||||||||
Db   476 GGTCAGTCGATCACAGTTCACAGCTCCGGCTGGGTGCTATAGGCGTGCCTTCAGGAAGTTA 417

Qy   175 TTGAAGGAGATGGAAAAGGGAAGCCTTTCGACGGAACA 212
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Db   416 TCGAAGGGGCTGGCAGGTGGAAGCTTTACTACAGAACA 379

Search completed: April 5, 2006, 22:24:01
Job time : 4982 secs

Dowell, P.
10/757356 Page 1
Seq ID 17

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 5, 2006, 20:42:51 ; Search time 3829 Seconds
(without alignments)
15825.312 Million cell updates/sec

Title: US-10-757-356-17
Perfect score: 1066
Sequence: 1 attcgccctggtgatttgga........atcgaagccgaaaaaaaaa 1066

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vi:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1066	100.0	1066	2	AY037769	Montastra
2	957.6	89.8	972	2	AY181554	Montastra
3	948.6	89.0	1045	2	AF406766	Montastra
4	914.8	85.8	1062	2	AY679109	Montastra
5	876	82.2	972	2	AY181555	Montastra
6	836.4	78.5	913	2	AY037768	Montastra
7	834.2	78.3	1046	2	AF401282	Montastra
8	681.2	63.9	729	11	AY182015	Synthetic
9	679.6	63.8	1045	2	AY181552	Montastra
10	678.4	63.6	836	2	AY181553	Montastra
11	665	62.4	1133	2	AY037766	Montastra
12	625.4	58.7	1046	2	AF384683	Montastra
13	624.8	58.6	684	2	AY679112	Montastra
14	623.2	58.5	684	2	AY679110	Montastra
15	621.8	58.3	708	11	AY182016	Synthetic
16	621.8	58.3	708	11	AY182021	Synthetic
17	610	57.2	967	2	AY181557	Montastra
18	604.2	56.7	708	11	AY182014	Synthetic
19	541.6	50.8	684	2	AB193294	Favia fav
20	533.4	50.0	795	2	AY037770	Montastra
21	527.2	49.5	684	2	AB193293	Favia fav
22	521.8	48.9	879	2	AY181556	Montastra
23	521.6	48.9	675	11	AB180726	Echinophy
24	513.6	48.2	702	11	AY182020	Synthetic
25	507.4	47.6	729	6	CS079401	Sequence
26	507.2	47.6	678	6	CS079393	Sequence
27	507	47.6	678	2	AY679111	Montastra
28	501	47.0	705	2	AY181558	Synthetic
29	499.2	46.8	702	11	AY182013	Synthetic
30	497.8	46.7	705	11	AY182018	Synthetic
31	497.4	46.7	705	11	CS079402	Sequence
32	497.4	46.7	678	6	CS079394	Sequence
33	489.2	45.9	702	11	AY182012	Synthetic
34	488	45.8	675	2	AY362545	Montastra
35	486.4	45.6	678	2	AB107915	Galaxea f
36	483.2	45.3	702	11	AB107915	Galaxea f
37	472	44.3	678	2	AY182019	Synthetic
38	469	44.0	705	11	AB108847	Galaxea f
39	467.2	43.8	675	6	AY182023	Synthetic
40	467.2	43.8	726	6	CS079392	Sequence
41	464	43.5	705	11	CS079400	Sequence
42	459.2	43.1	675	2	AY182017	Synthetic
43	456.2	42.8	705	11	AY056460	Montastra
44	454	42.6	681	2	AY182022	Synthetic
45	437.4	41.0	5070	11	AY765217	Lobophyll
					AY585853	PsiSTRIKE

ALIGNMENTS

RESULT 1
AY037769
LOCUS   AY037769   1066 bp   mRNA   linear   INV 05-APR-2002
DEFINITION Montastraea cavernosa mcavFP_6 mRNA, complete cds.
ACCESSION   AY037769
VERSION   AY037769.1 GI:19982568
KEYWORDS
SOURCE   Montastraea cavernosa (great star coral)
  ORGANISM Montastraea cavernosa
            Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Scleractinia;
            Faviina; Faviidae; Montastraea.
REFERENCE   1 (bases 1 to 1066)
  AUTHORS   Labas,Y.A., Gurskaya,N.G., Yanushevich,Y.G., Fradkov,A.F.,
            Lukyanov,K.A., Lukyanov,S.A. and Matz,M.V.
  TITLE   Diversity and evolution of the green fluorescent protein family
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (7), 4256-4261 (2002)
   PUBMED   11929996
REFERENCE   2 (bases 1 to 1066)
  AUTHORS   Matz,M.V. and Lukyanov,S.A.
  TITLE   Direct Submission
  JOURNAL   Submitted (30-MAY-2001) Institute of Bioorganic Chemistry RAS,
            Miklukho-Maklaya 16/10, Moscow 117871, Russia
FEATURES   Location/Qualifiers
     source   1..1066
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                     /mol_type="mRNA"
                     /db_xref="taxon:63558"
     CDS   81..785
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                     /codon_start=1
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                     /protein_id="AAK71335.1"
                     /db_xref="GI:19982569"
                     /translation="MTSVAQBKGVIKPDMKMKLRMEGAVNGHKPVVEGDGKGKPFDGT
                     QTMDLTVIEGAPLPFAYDILTVFDYGNRVFAKYPEDIADYFKQTFPEGYFWERSMTY
                     EDQGICIATNDITMWEGVDDCFAYKIRFDGVNFPANGPVMQRKTLKWEPSTEIMYARD
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                     LHEHABEARHGLSRKAK"
ORIGIN

Query Match   100.0%; Score 1066; DB 2; Length 1066;

Db   1021 AAAACTGTAGTGAGAATAAACTTGTTATCGAAGCCGAAAAAAAAAA 1066

RESULT 2
AY181554
LOCUS   AY181554   972 bp   mRNA   linear   INV 25-JUN-2003
DEFINITION Montastraea cavernosa isolate mc3 green fluorescent protein mRNA,
            complete cds.
ACCESSION   AY181554
VERSION   AY181554.1 GI:32188169
KEYWORDS   .
SOURCE   Montastraea cavernosa (great star coral)
  ORGANISM Montastraea cavernosa
            Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Scleractinia;
            Faviina; Faviidae; Montastraea.
REFERENCE   1 (bases 1 to 972)
  AUTHORS   Kelmanson,I.V. and Matz,M.V.
  TITLE   Molecular Basis and Evolutionary Origins of Color Diversity in
            Great Star Coral Montasraea cavernosa (Scleractinia: Favida)
  JOURNAL   Mol. Biol. Evol. 20 (7), 1125-1133 (2003)
   PUBMED   12777529
REFERENCE   2 (bases 1 to 972)
  AUTHORS   Kelmanson,I.V. and Matz,M.V.
  TITLE   Direct Submission
  JOURNAL   Submitted (17-NOV-2002) Whitney Laboratory, University of Florida,
            9505 Ocean Shore Blvd, St Augustine, FL 32080, USA
FEATURES   Location/Qualifiers
     source   1..972
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     CDS   81..785
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                     /db_xref="GI:32188170"
                     /translation="MTSVAQEKGVIKPDMKMKLRMEGAVNGHKFVIEGDGKGKPFDGT
                     QTMDLTVIRGAPLPFAYDILTTVFDYGNRVFAKYPEDIADYFKQTPEGYFWERSMTY
                     EDQGICIATNDITMKGVDDCFVYKIRFDGVNFPANGPVMQRKTLKWEPSTEIMYVRD
                     GVLKGDVNMALLLEGGGHYRCDFKTTYKAKKVVRLPDYHFVDHRIEIVSHDKDYNKVK
                     LHEHAEARHGLSRKAK"

ORIGIN

Query Match   89.8%; Score 957.6; DB 2; Length 972;
Best Local Similarity 99.1%; Pred. No. 7.1e-259;
Matches 963; Conservative   0; Mismatches   9; Indels   0; Gaps   0;

Qy   1 ATTCGCCCTGGTGATTGGAAGAGAGCAGATCGAGACAACAAGAGCTGTAAGGTTGATA 60
          |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATTCACCCTGGTGATTGGAAGAGAGCAGATCGAGACAACAAGAGCTGTAAGGTTGATA 60

Qy   61 TCTTACTTACGTCTACCATCATGACAAGTGTTGCACAGGAAAAGGGTGTGATTAAACCAG 120
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Db   61 TCTTACTTACGTCTACCATCATGACAAGTGTTGCACAGGAAAAGGGTGTGATTAAACCAG 120

Qy   121 ACATGAAGATGAAGCTGCGTATGGAAGGTGCTGTAAACGGGCACAAGTTCGTGGTTGAAG 180
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Db   121 ACATGAAGATGAAGCTGCGTATGGAAGGTGCTGTAAACGGGCACAAGTTCGTGGTTGAAG 180

Qy   181 GAGATGGAAAAGGGAAGCCTTTCGACGGAACAGAGACTATGGACCTTACAGTCATAGAAG 240
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Db   181 GAGATGGAAAAGGGAAGCCTTTCGACGGAACAGAGACTATGGACCTTACAGTCATAGAAG 240

Qy   241 GCGCACCATTGCCTTTCGCTTACGATATCTTGACAACAGTATTCGATTACGGCAACAGGG 300
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Db   241 GCGCACCATTGCCTTTCGCTTACGATATCTTGACAACAGTATTCGATTACGGCAACAGGG 300

Qy   301 TATTCGCCAAATACCCAGAAGACATAGCAGATTATTTCAAGCAGACGTTTCCTGAGGGGT 360
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Db   301 TATTCGCCAAATACCCAGAAGACATAGCAGATTATTTCAAGCAGACGTTTCCTGAGGGGT 360

Qy   361 ACTTCTGGGAACGAAGCATGACATACGAAGACCAGGGCATTTGCATCGCCACAAACGACA 420

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Db   361 ACTTCTGGAACGAACGATGACATACGAAGACCAGGCATTTGCCTATAAAATTCGATTTGATGGTGTGA 420
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Qy   421 TAACAATGATGAAGGCGTCGACGACTGTTTTGTCTATAAATTCGATTTGATGGTGTGA 480
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Db   421 TAACAATGATGAAGGCCGTCGACGACTGTTTTGTCTATAAATTCGATTTGATGGTGTGA 480

Qy   481 ACTTTCCTGCCAATGGTCCAGTTATGCGAGAGACGCTGAAATGGGAGCCATCCACTG 540
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Db   481 ACTTTCCTGCCAATGGTCCAGTTATGCGAGAGACGCTGAAATGGGAGCCATCCACTG 540

Qy   541 AGATAATGTATGCGCGTGATGGAGTGCTGAAGGGTGAAGGGTGATGTTAACATGGCTCGTTGCTTG 600
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Db   541 AGATAATGTATGCGCGTGATGGAGTGCTGAAGGGTGAAGGGTGATGTTAACATGGCTCGTTGCTTG 600

Qy   601 AAGGAGGTGGCCATTACCGATGTGACTTCAAAACTACTTACAAAGCTAAGAAGGTTGTCC 660
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 AAGGAGGTGGCCATTACCGATGTGACTTCAAAACTACTTACAAAGCTAAGAAGGTTGTCC 660

Qy   661 GGTTGCCAGACTATCACTTTGTGGACCATGCCGATTGTGAGCGCCACGACACAAAGATT 720
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Db   661 GGTTGCCAGACTATCACTTTGTGGACCATGCCGATTGTGAGCGCCACGACACAAAGATT 720

Qy   721 ACAACAAGGTTAAGCTGCACGACCATGCCGCGAAGCTCGTCGAGGACTGTTCAAGGAGGCCA 780
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Db   721 ACAACAAGGTTAAGCTGCACGACCATGCCGCGAAGCTCGTCGAGGACTGTTCAAGGAGGCCA 780

Qy   781 AGTAAAGGCTTAATGAAAAGTCAAGAACGACGAGGAGAAACAAAGTACTTTTTGTTA 840
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 AGTAAAGGCTTAATGAAAAGTCAAGAACGACGAGGAGAAACAAAGTACTTTTTGTTA 840

Qy   841 AATTTGAAGGCATTTACTCGGAATTAGTATTTGATACTTTCGATTCAAGGATTTGTTCCAGTTTT 900
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Db   841 AATTTGAAGGCATTTACTCGGAATTAGTATTTGATACTTTCGATTCAAGGATTTGTTTCG 900

Qy   901 GGATTTGTTGAGAGACTAGCTAGCTCTAGAGTTGTATTTTGTGAAAAAGAAGATAGTTTCCAGTTTT 960
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 GGATTTGTTGAGAGACTAGCTAGCTCTAGAGTTGTATTTTGTGAAAAAGAAGATAGTTTCCAGTCTT 960

Qy   961 TGCGGGATTACA 972
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Db   961 TGCGGGATTACA 972
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RESULT 3
AF406766
LOCUS       AF406766                1045 bp    mRNA    linear   INV 04-SEP-2001
DEFINITION  Montastraea cavernosa green fluorescent protein mRNA, complete cds.
ACCESSION   AF406766
VERSION     AF406766.1  GI:15425964
KEYWORDS    .
SOURCE      Montastraea cavernosa (great star coral)
  ORGANISM  Montastraea cavernosa
            Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Scleractinia;
            Faviina; Faviidae; Montastraea.
REFERENCE   1  (bases 1 to 1045)
  AUTHORS   Lesser,M.P., Barry,T.M., Mazel,C., Matz,M.V., Lukyanov,S.A.,
            Falkowski,P., Gorbunov,M. and Kolber,Z.
  TITLE     Green Fluorescent Proteins in Caribbean Scleractinian Corals
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1045)
  AUTHORS   Lesser,M.P. and Barry,T.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-AUG-2001) Department of Zoology and Center for Marine
            Biology, University of New Hampshire, 46 College Road, Durham, NH
            03824, USA
FEATURES             Location/Qualifiers
     source          1..1045
                     /organism="Montastraea cavernosa"
                     /mol_type="mRNA"
                     /db_xref="taxon:63558"
                     /note="isolated from specimen with red color"
     CDS             84..767
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                     /codon_start=1
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                     /protein_id="AAK97633.1"
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                     IEGAPLPFAYDILTVFDYGNRVFAKYPQDITDYFKQTFPEGYFWERSMTYEDQGICI
                     ATNDITMMKGVDDCFVYKIRFDGVNFPANGPVMQRKTLKWEPSTEIMYARDGVLKGDV
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                     XXGLsRKAK"

ORIGIN

Query Match      89.0%;  Score 948.6;  DB 2;  Length 1045;
Best Local Similarity  95.2%;  Pred. No. 2.5e-256;
Matches 1014;  Conservative 4; Mismatches 23;  Indels 24; Gaps  3;
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Qy    1 ATTCGCCCTGGATTGGAAGAGAGGAGATCGAAGACAACAAGAGCTG--TAAGGTTGA 58
        ||||||| ||||||||||||||||||||||||||||||||||||||  ||||||||||
Db    2 ATTCGCCCTGGTGATTGGAAGAGAGCAGATCAAGACAACAAGAGCTGTATAAGGTTTA 61

Qy   59 TATCTTACTTACGTCTACCATCATGACAAGTGTTGCACAGGAAAAGGGTGTGATTAAACC 118
        |||||||||||||||||||||||||      |||||||||
Db   62 TATCTTACTTACGTCTACCGTCATGA------------GTGTGATAAAACC 100

Qy  119 AGACATGAAGATGAAGCTGCGTATGGAAGGTGCTGTAAACGGGCACAAGTTCGTGGTTGA 178
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  101 AGACATGAAGATCAAGCTGCGTATGGAAGGCGCTGTAAACGGGCACAAGTTCGTGATTGA 160

Qy  179 AGGAGATGGAAAAGGGCAAGCCTTCGACGACAACAGACTTATGGGACCTTACAGTCATAGA 238
        |||||| |||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db  161 AGGAGACGGAAAAGGGCAAGCCTTCGAAGGGAACAAGACTATGGGACCTTACAGTCATAGA 220

Qy  239 AGGGCCACCATTGCCTTTGCCTTACGATATCTTGACAACATCTTGACAACAAGTATTCGATTACGGCAACAG 298
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Db  221 AGGGCGACCACTGCCCTTTGCCTTACGATATCTTGACAACATCTTGACAACAAGTATTCGATTACGGCAACAG 280

Qy  299 GGTATTCGCCAAATACCCAGAAGACATGACATACGAAGACCAGGGCATTTGCATCGCCACAAACGA 358
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  281 GGTATTCGCCAAATACCCAGAAGACATGACATACGAAGACCAGGGCATTTGCATCGCCACAAACGA 340

Qy  359 GTACTTCTGGGAACGAACGATGACATACGAAGACCAGGGCGATTTGCCTATAAAATTCGATTTGATGTGT 418
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Db  341 GTACTTCTGGGAACGAACGATGACATACGAAGACCAGGGCGATTTGCCTATAAAATTCGATTTGATGTGT 400

Qy  419 CATAACAATGATGAAGGCGTCGACGACTGTTTTGTCTATAAATTCGATTTGATGTGT 478
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Db  401 CATAACAATGATGAAGGCGTCGACGACTGTTTTGTCTATAAATTCGATTTGATGTGT 460

Qy  479 GAACTTTCCTGCCAATGGTCCAGTTATGCAGAGAAGACGCTGAAATGGGAGCCATCCAC 538
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  461 GAACTTTCCTGCCAATGGTCCAGTTATGCAGAGAAGACGCTGAAATGGGAGCCATCCAC 520

Qy  539 TGAGATAATGTATGCGCGTGATGGAGTGCTGAAGGGTGATGTTAACATGGCTCTGTGTGCT 598
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Db  521 TGAGATAATGTATGCGCGTGATGGAGTGCTGAAGGGTGATGTTAACATGGCTCTGTGTGCT 580

Qy  599 TGAGGAGGTGGCCATTACCGATGTGACTTCAAAACTACTTACAAAGCTAAGAAGGTTGT 658
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Db  581 TGAGGAGGTGGCCATTACCGATGTGACTTCAAAACTACTTACAAAGCTAAGAAGGTTGT 640

Qy  659 CCGGTTGCCAGACTATCACTTTGTGGACCATTGTGAGATTGTGAGCCACGACGACAAAGA 718
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Db  641 CCGGTTGCCAGACTATCACTTTGTGGACCATTGTGAGATTGTGAGCCACGACGACAAAGA 700

Qy  719 TTACAACAAGGTTAAGCTGCACGACCATGCCGAAGCTCGTCATGGACTGTCAAGGAGGC 778
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Db  701 TTACAACAAGGTTAAGCTGCGTATGAGCATGCCGAAGCTCRCRCMTGGACTGTCRAGGAAGGC 760

Qy  779 CAAGTAAAGGCTTAATGAAAAGTCAAGAACGACGAGGAGAAACA--AAGTACTTTTTTG 837
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Db  761 CAAGTAAAGGCTTAATGAAAAGTCAAGAACGACGACGACAAGTAGTTTTTG 820

Qy  838 TTAAATTTGAAGGCATTTACTCGGAATTAGTATTTGATACTTTCGATTCAAGGATTTGTT 897
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Qy    179  AGGAGGATGGAAAAGGAAGCCTTTCGACGGAACAGACTCATGAGACCTTACAGTCATAGA  238
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Db    160  AGGAGACGGAAAAGCCAAGCCTTTCGAGGGAAAAACAGACTCATGAGACCTTACAGTCATAGA  219

Qy    239  AGGCGCACCATTGCCTTCGCTTAGATATCTTGACAACAGTATTCGATTACGGCAACAG  298
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Db    220  AGGCGCACCTTTGCCTTCGCTTACATATCTTGACAACAGTATTCGATTACGGCAACAG  279

Qy    299  GGTATTCGCCAAATACCCAGCAGAGCACATAGCAGAGATTATTTCAGCAGACGTTTCCTCGAGGG  358
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Db    280  GGTATTCGCCAAATACCCAAAAGACATACCAAGACTATTTCAGCAGACGTTTCCGGAGGG  339

Qy    359  GTACTTCTGGAACGAAGCATGACATACGAGAACCAGGGCATTGCATCGCCACAAACGA  418
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Db    340  GTACTTCTGGAACGAAGCATGACATACGAGAACCAGGGCATTGCATCGCCACAAACGA  399

Qy    419  CATAACAATGATGGAAGGGCGTCGACGACTGTTTGCCTATAAAATTCGATTTGATGGTGT  478
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Db    400  CATAACAATGATGAAAGGCGTCGACGACTGTTTGTCTATAAAAATTCGATTTGATGGTGT  459

Qy    479  GAACTTCCTGCCAATGGTCCAGTTATGCAGAGGAGACGCGTGAAATGGGAGCCATCCAC  538
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    460  GAACTTCCTGCCAATGGTCCAGTTATGCAGAGGAGACGCTAAAATGGGAGCCATCCAC  519

Qy    539  TGAGATAATGTATGCGCGTGATGAGTGCTGAAGGGTGAATGGCTCTGTTGCT  598
           |||||| ||||||||| |||||||||||||| |||||||||||||||||||||
Db    520  TGAAAAATGTATGTGCGTGATGGGGTACTGGAGGGTGATGGGTGTAACATGGCTCTGTTGCT  579

Qy    599  TGAAGGAGGTGGCCATTACCGATGTGACTTCAAAACTACTTACAAAGCTAAGAAGGTTGT  658
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Db    580  TGAAGGAGGTGGCCATTACCGATGTGACTTCAAAACTACTTACAAAGCTAAGAAGGTTGT  639

Qy    659  CCGGTTGCCAGACTATCACTTGTCGACCATCGCATTGAGATTGTGAGCCACGACAAAGA  718
           ||||||||||||||||||||| ||||||||||||||||||||||||| |||||||||||
Db    640  CCAGTTGCCAGACTATCATTTGTTGACCATCGCATTGAGATTGTGAGCCCCGACAAAGA  699

Qy    719  TTACACAAAGGTTAAGCTGCACGAGCATGCCGAAGCTCGTCATGGACTCGTCAAGGAGAGGC  778
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Db    700  TTACACAAAGGTTAAGCTGTATGAGCATGCCGAAGCTCATTTGGGCTGCCGAGGCAGGC  759

Qy    779  CAAGTAAAGGCTTAATGAAAAGTCAAGACGACAAGGAGGAGAAACAAAGTACTTTTTTGT  838
           |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db    760  CAAGTAAAGGCTTAATGAAAAGCCAAGACGACAAGGAGGAGAAACAAAGTATTTTTTTGT  819

Qy    839  TAAATTTGAAGGCATTTACTCGGAATTAGTATTTCGATTCAAGGATTTGTTC  898
           |||||| ||||||||||||||||||| |||||||||||||||||||||||||||
Db    820  TAAATTGGAAGGCATTTACTCGGAATTAGTATTTGATACTTTCGATTCAAGGATTTGTT  879

Qy    899  CGGGATTGTTGTAGAGACTAGCTCTAGAGTTGTATTTTGTATTTTGTGAAAAAGATAGTTTCCAGTT  958
           |||||||| ||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db    880  CGAGATTTTTTANAGACTAGCTNTANAGTGTATTTTGTATTTGTGAAAAAANATAGTTTCCAGTT  939

Qy    959  TTTGCGGGATTACAGCATGGGATAGACTTTTTAAACTCAGTTGTGGTCAAATGCAAGTA  1018
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Db    940  TTTGCGGGACTACAGCATAGGGATAGACCTTTTAAACTCAGTTGTGGTCAAATACAAGTA  999

Qy   1019- AGAAAACTGTAGTGAGAATAAACTTGTTATCGAAGCCGAAAAAAAA  1066
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Db   1000  AGAAAACTGTAGTGAGAATAAACTTGTTGTCGAAAAAAAAAAAAAAA  1047
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RESULT 5
AY181555
LOCUS       AY181555                 972 bp    mRNA    linear    INV 25-JUN-2003
DEFINITION  Montastraea cavernosa isolate mc4 green fluorescent protein mRNA,
            complete cds.
ACCESSION   AY181555
VERSION     AY181555.1  GI:32188171
KEYWORDS    .
SOURCE      Montastraea cavernosa (great star coral)
  ORGANISM  Montastraea cavernosa
            Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Scleractinia;
            Faviina; Faviidae; Montastraea.
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Db    821  TTAAATTGGAAGGCATTTACTCGGAATTAGTATTTCGATTCAAGGATTTGTT  880
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Qy    898  CCGGGATTGTTGTAGAGACTAGCTCTAGAGTTGTATTTTGTGAAAAAGATAGTAGTTTCCAGT  957

Db    881  TCGGGATTGTTGTAGAGACTAGCTCTAGAGTTGTATTTTGTGAAAAAGATAGTAGTTTCCAGT  940

Qy    958  TTTTGCGGGATTACAGCATGGGATAGAATAAACTGTTATCGAAGCGAAAAAGT  1017
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Db    941  TTTTGCGGGATTACAGCATGGGATAGACTTTTTAAACTCAGTTGTGGTCAAATGCAAGT  1000

Qy   1018  AAGAAAACTGTAGTGAGAATAAACTGTTATCGAAGCCGAAAAAA  1062
           |||||||||||||||||||||||||| ||||||||||||||
Db   1001  AAGAAAACTGTAGTGAGAATAAACTTGTTATCGAAGCCGAAAAAA  1045
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RESULT 4
AY679109
LOCUS       AY679109                1062 bp    mRNA    linear    INV 25-AUG-2004
DEFINITION  Montastraea cavernosa green fluorescent protein G1 mRNA, complete
            cds.
ACCESSION   AY679109
VERSION     AY679109.1  GI:51472050
KEYWORDS    .
SOURCE      Montastraea cavernosa (great star coral)
  ORGANISM  Montastraea cavernosa
            Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Scleractinia;
            Faviina; Faviidae; Montastraea.
REFERENCE   1  (bases 1 to 1062)
  AUTHORS   Carter,R.W., Gibbs,P.D.L. and Schmale,M.C.
  TITLE     Cloning of Cnidarian Fluorescent Protein Genes
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1062)
  AUTHORS   Carter,R.W., Gibbs,P.D.L. and Schmale,M.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-JUL-2004) MBF, University of Miami, 4600 Rickenbacker
            Cswy, Miami, FL 33129, USA
FEATURES             Location/Qualifiers
     source          1..1062
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                     /mol_type="mRNA"
                     /db_xref="taxon:63558"
     5'UTR           1..82
     CDS             83..766
                     /note="GFP-like; McaG1"
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                     /protein_id="AAU04446.1"
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                     HFGLPRQAK"
     3'UTR           767..1062
     polyA_signal    1016..1021
ORIGIN
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Query Match             85.8%;  Score 914.8;  DB 2;  Length 1062;
Best Local Similarity   92.6%;  Pred. No. 8.7e-247;
  Matches  989;        Conservative    0;  Mismatches  56;  Indels  23;  Gaps  2;

Qy      1  ATTCGGCCCTGGTGATTTGGAGAGAGCAGATCGAGAACAACAAGAGCTG--TAAGGTTGA  58
           || ||||| |||||||||||||||||||||| ||||||||||||||||||||  ||||||||
Db      1  ATTCACCCTGGTGATTTGGAGAGAGCAGATCGAGAACAACAAGAGCTGTATAAGGTTGA  60

Qy     59  TATCTTACTTACGTCTACCATCATGACAAGTGTTGCACAGAGAAAAGGGTGTGATTAAACC  118
           ||||||||||||||||||||||||||||||||||||||||||||          ||||||||||
Db     61  TATCTTACTTACGTCTACCGTCATGA-----------------GTGTGATAAAACC  99

Qy    119  AGACATGAAGATGAAGCTGCGTATGGAAGGTGCTGTGAAGGTCGGCCACAAGTTCGTGGTTGA  178
           |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db    100  AGACATGAAGATCAAGCTGCGTATGGAAGGTGCTGTGAATGGCCACAAGTTCGTGATTGA  159
```

REFERENCE   1 (bases 1 to 972)
AUTHORS   Kelmanson,I.V. and Matz,M.V.
TITLE   Molecular Basis and Evolutionary Origins of Color Diversity in
             Great Star Coral Montastraea cavernosa (Scleractinia: Favida)
JOURNAL   Mol. Biol. Evol. 20 (7), 1125-1133 (2003)
PUBMED   12777529
REFERENCE   2 (bases 1 to 972)
AUTHORS   Kelmanson,I.V. and Matz,M.V.
TITLE   Direct Submission
JOURNAL   Submitted (17-NOV-2002) Whitney Laboratory, University of Florida,
             9505 Ocean Shore Blvd, St Augustine, FL 32080, USA
FEATURES   Location/Qualifiers
     source   1..972
                     /organism="Montastraea cavernosa"
                     /mol_type="mRNA"
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     CDS   77..760
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                     /product="green fluorescent protein"
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                     ATNDITMKGVDDCFLYKIRFDGVNFPANGPVMQRKTLKWEPSTEKMYYRVRDGVLKGDV
                     NMALLEGGHYRCDFKTTYKAKKVVQLPDYHFVDHRIEIVSHDKDYNKVKLYEHAEA
                     HSGLPRQAK"
ORIGIN

Query Match   82.2%; Score 876; DB 2; Length 972;
Best Local Similarity   93.9%; Pred. No. 7.8e-236;
Matches 931; Conservative   0; Mismatches 40; Indels 21; Gaps   1;

Qy   6 CCCTGGTGATTTGGAAGAGAGCAGATCGAAGAGCAGAAACAAGAGCTGTAAGGTTGATATCTTA 65
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2 CCCTGGTGATTTGGAAGAGAGCAGATCGAAGAGCAGAAAACAAGAGCTGTAAGGTTGATATCTTA 61

Qy   66 CTTACGTCTACCATCATGACAAGTGTTGCACAGAGAAAAGGGTGTGATTAAACCAGACATG 125
            ||||||||||||||||||||||| |||||||||||||||||||||
Db   62 CTTACGTCTACAATCATGA-----------------GTGTGATAAAGCCAGACATG 100

Qy   126 AAGATGAAGCTGCCTATGGAAGGTGCTGTAAACGGGCACAAGTTCGTGTTGAAGGAGAT 185
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   101 AAGATCAAGCTGCCTATGGAAGGTGCTGTAAACGGGCACAAGTTCGTGATTGAAGGAGAC 160

Qy   186 GGAAAAGGGAAGCCTTTCGACGGAACACAGACTATGGACCTTACAGTCATAGAAGGCGCA 245
            ||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db   161 GGAAAAGGCAAGCCTTTCGAGGGAAAACAGACTATGGACCTTACAGTCATAGAAGGCGCA 220

Qy   246 CCATTGCCTTTCGCTTACGATATCTTGACAACAGTATTCGATTACGGCAACAGGGTATTC 305
            |||||||||| ||||||||||||| |||||||||||||||||||||||||||||||||
Db   221 CCTTTGCCTTTCGCTTACGATATCTTGACAACAGTATTCGATTACGGCAACAGGGTATTC 280

Qy   306 GCCAAATACCCAGAGACATAGAGATTATTTCAAGCACGACGTTTCCTGAGGGGTACTTC 365
            ||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db   281 GCCAAATACCCAAAAGACATACCAGATTATTTCAAGCACGACGTTTCCTGAGGGGTACTCC 340

Qy   366 TGGGAACGAAGCATGACATACGAAGACCAGGGCATTTGCATCGCCACAAACGACATAACA 425
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   341 TGGGAACGAAGCATGACATACGAAGACCAGGGCATTTGCATCGCCACGACGACATAACA 400

Qy   426 ATGATGGAAGGCGTCGACGACTGTTTTGCCTATAAAAATTCGATTTGATGGTGTGAACTTT 485
            ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db   401 ATGATGAAAGGCGTCGATGAGTGTTTTCTCTATAAAAATTCGATTTGATGGTGTGAACTTT 460

Qy   486 CCTGCCAATGGTCCAGTTATGCAGAGAAGACCGCTGAAATGGAGCCATCCACTGAGATA 545
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   461 CCTGCCAATGGTCCAGTTATGCAGAGAAGACCGCTGAAATGGAGCCATCCACTGAGATA 520

Qy   546 ATGTATGCGCGTGATGGAGTGCTGAAGGGTGATGTTAACATGGCTCTCGTTGCTTGAAGGA 605
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   521 ATGTATGCCGTGATGGAGTGCTGAAGGGTGATGTTAACATGGCTCTCGTTGCTTGAAGGA 580

RESULT 6
AY037768
LOCUS   AY037768   913 bp   mRNA   linear   INV 31-MAY-2002
DEFINITION Montastraea cavernosa clone 7.7 green fluorescent protein-like
            protein mRNA, complete cds.
ACCESSION   AY037768
VERSION   AY037768.1 GI:21303777
KEYWORDS   .
SOURCE   Montastraea cavernosa (great star coral)
  ORGANISM Montastraea cavernosa
            Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Scleractinia;
            Favina; Faviidae; Montastraea.
REFERENCE   1 (bases 1 to 913)
  AUTHORS   Matz,M.V. and Lukyanov,S.A.
  TITLE   Diversity and evolution of GFP-like fluorescent proteins
  JOURNAL   Unpublished
REFERENCE   2 (bases 1 to 913)
  AUTHORS   Matz,M.V. and Lukyanov,S.A.
  TITLE   Direct Submission
  JOURNAL   Submitted (30-MAY-2001) Institute of Bioorganic Chemistry RAS,
            Miklukho-Maklaya 16/10, Moscow 117871, Russia
FEATURES   Location/Qualifiers
     source   1..913
                     /organism="Montastraea cavernosa"
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                     /clone="7.7"
     CDS   38..742
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                     GVLKGDVNMALLLEGGGHYRDXKTTYRAKKVVQLPDYHFVDHRIEIVSHDKDYNKVK.
                     LYEHAEAHSGLPRQAK"
ORIGIN

Query Match   78.5%; Score 836.4; DB 2; Length 913;
Best Local Similarity   .96.2%; Pred. No. 1.2e-224;
Matches 860; Conservative   6; Mismatches 27; Indels 1; Gaps   1;

Qy   606 GGTGGCCATTACCGATGTGACTTCAAAATACTTACAAGTCAAGAAGGTTGTCCGGTTG 665
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   581 GGTGGCCATTACCGATGTGACTTCAAAATACTTACAAGTCAAGAAGGTTGTCCAGTTG 640

Qy   666 CCAGACTATCACTTTGTGGACCATGCCATTGAGATTGTGAGCCACCAGATTACAAC 725
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   641 CCAGACTATCATTTTGTGGACCATGCCATTGAGATTGTGAGCCACCAGATTACAAC 700

Qy   726 AAGGTTAAGCTGCACGAGCATGCCGAGCCGAGCTCGTCATGGACTGTCAAGGAAGGCCAAGTAA 785
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   701 AAGGTTAAGCTGTATGAGCATGCCGAGCTCATTCTGGGCTGCCGAGGCAGGCCAAGTAA 760

Qy   786 AGGCTTAATGAAAGTCAAGACGACACAAGGAGAAACAAAGTACTTTTTTGTTAAATT 845
            ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db   761 AGGCTTAATGAAAGCCAAGACGACAACAAGGAGAAACAAAGTATTTTTTGTTAAATT 820

Qy   846 GAAGGCATTTACTCGGAATTAGTATTTGATACTTTCGATTCAAGGATTTGTTCCGGGATT 905
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   821 CAAGGCATTTACTCGGAATTAGTATTTGATATTTCGATTCAAGGATTTGTTCGGGATT 880

Qy   906 TGTTAGAGACTAGCTCTAGAGTTGTGTATTTGTATTTGTGAAAAAAGATAGTTTCCAGTTTTTGCGG 965
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   881 TGTTAGAGACTAGCTCTAGAGTTGTGTATTTGTATTTGTGAAAAAAGATAGTTTCCATTTTTTGCGG 940

Qy   966 GATTACAGCATGGGGATAGACTTTTTAAACTC 997
            ||||||||||||||||||||||||||||||
Db   941 GATTACAGCATAGGGATAGACTTTTTAAACTC 972

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AUTHORS      Lesser,M.P., Barry,T.M., Mazel,C., Matz,M.V., Lukyanov,S.A.,
             Falkowski,P., Gorbunov,M. and Kolber,Z.
TITLE        Green Fluorescent Proteins in Caribbean Scleractinian Corals
JOURNAL      Unpublished
REFERENCE    2 (bases 1 to 1046)
AUTHORS      Lesser,M.P. and Barry,T.M.
TITLE        Direct Submission
JOURNAL      Submitted (20-JUL-2001) Department of Zoology and Center for Marine
             Biology, University of New Hampshire, 46 College Road, Durham, NH
             03824, USA
FEATURES             Location/Qualifiers
     source          1..1046
                     /organism="Montastraea faveolata"
                     /mol_type="mRNA"
                     /db_xref="taxon:48498"
     CDS             84..767
                     /codon_start=1
                     /product="green fluorescent protein"
                     /protein_id="AAK83923.1"
                     /db_xref="GI:15081472"
                     /translation="MSVIKPDMKIKLRMEGAVNGHKFVIEGDGKGKPEGTQSMDLTV
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                     ATNDITLMKGVDDCFVYKIRFDGVNFPANGPVMQKKTLKWEPSTEKMYVRDGVLKGDV
                     NMALLLEGGGHYRCDFKTTYKAKKFVQLPDYHFVDHRIEILSHDKDYNKVKLYEHAEA
                     HSGLPRQAK"
ORIGIN
Query Match      78.3%;  Score 834.2;  DB 2;  Length 1046;
Best Local Similarity   89.9%;  Pred. No. 5e-224;
Matches  961;  Conservative   0;  Mismatches   78;  Indels   30;  Gaps   5;

Qy         1 ATTCGCCCTGGTGATTTGGAAGAGAGCAGATCGAGAACAACAAGAGCTG--TAAGGTTGA  58
             ||||||||||||||||||||||||||||||||||||||||||||||||||  ||||||||
Db         2 ATTCGCCCTGGTGATTTGGAAGAGAGCAGATCGAGAACAACAAGAGCTGTATAAGGTTTA  61

Qy        59 TATCTTACTTACGTCTACCATCATGACAAGTGTTGCACAGGAAAAGGGTGTGATTAAACC  118
             ||||||||||||||||||||||||||||||||||      |||||||||||||||||||
Db        62 TATCTTACTTACGTCTACCATCATGACAAGTGTTGCACAGGA------GTGTGATAAAACC  100

Qy       119 AGACATGAAGATGAAGAGCTGCTATGGAAGGTGCTGTAAACGGGCACAAGTTCGTGGTTGA  178
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       101 AGACATGAAGATGAAGAGCTGCTATGGAAGGTGCTGTAAACGGGCACAAGTTCGTGGATTGA  160

Qy       179 AGGAGATGAAAAGGGAAGGCCTTTCGACGGAACACAGACTTTACAGTCATAGA  238
             |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       161 AGGAGACGGAAAGGGCAAGCCTTTCGACGGAACACAGACTTTACAGTCAAAGA  220

Qy       239 AGGCGCACCATTGCCTTCGCTTACGATATCTTGACAACAGTATTCGCAACAG  298
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       221 AGGCGCGCCTCTGCCTTTGCTTACGATATCTTGACAACAGTATTCGACAACAG  280

Qy       299 GGTATTCGCCAAATACCCAGAAGACATGACATACGAAGACCAGGGCATTTCGATTCAAGG  358
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       281 GGTATTTGCCAAATACCCACCAAGATATACCAGACTCATTTCGATTCAAGG  340

Qy       359 GTACTTCTGGGAACGAAGCATGACATACGAAGACCAGGGCATTGCATCGCCACAAACGA  418
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       341 GTATTCCTGGGAACGGAGCATGACATACGAAGACCAGGGCATTGCCTCGCCGCCACAAACGA  400

Qy       419 CATAACAATGATGATGAAGAGGCGTCGACGACTGTTTGCCTATAAAATTCGATTTGATGTGT  478
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       401 CATAACACTGATGAAGAGGCGTCGACGACTGTTTGTCTATAAAATTCGATTTGATGGTGT  460

Qy       479 GAACTTCCTGCCAATGGTCCAGTTATGCAGAGGAAGACGCTGAAATGGGAGCCATCCAC  538
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       461 AAACTTCCTGCCAATGGTCCAGTTATGCAGAAAGAGACGCGCTGAAATGGGAGCCATCCAC  520

Qy       539 TGAGATAATGTATGCGCGTGAGGTGCTCAAGGTGATGTTAACATGGCTCTGTTGCT  598
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       521 TGAGAAATGTATGTGCGTGAGGTGCTCAAGGTGATGTTAACATGGCTCTGTTGCT  580

Qy       599 TGAAGGAGGTGGCCATTACCGATGCGACTTCAAAACTACTTACAAAGCTAAGAAGGTTGCT  658
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   52 AGGTTGATATCTTACTTACGTCTACCATCATGACAAGTGTGCACAGGAAAAGGGTGTGA 111
             |||||||||
Db   9 AGGGTGATATCTTACTTACGTCTACCATCATGACCAGACCAGTGTGCACAGGAAAAGGGTGTGA 68

Qy   112 TTAAACCAGACATGAAGATGAAGAGCTGCGTATGGAAGGTGCTGTAAACGGGCACAAGTTCG 171
             |||||||||
Db   69 TTAAACCAGACATGAAGATGAAGAGCTGCGTATGGAAGGTGCTGTAAACGGGCACAAGTTCG 128

Qy   172 TGGTTGAAGGAGATGGAAAAGGGAGAAAGGGGAAGCCTTTCGACGGAACACAGACTTACAG 231
             |||||||||
Db   129 TGATTGAAGGAGATGGAAAAGGGAGAAAGGGGAAGCCTTTCGACGGAACACAGACTTACAG 188

Qy   232 TCATAGAAGGCGCACCATTGCCTTCGCTTACGATATCTTGACACAGTATTCGATTACG 291
             |||||||||
Db   189 TCATAGAAGGCGCGCCACCATTGCCTTTCGCTTACGATATCTTGACAACAGTATTCGATTACG 248

Qy   292 GCAACAGGGTATTCGCCAAATACCCAGAAGACATAGCAGATTATTTCAAGCAGACGTTTC 351
             |||||||||
Db   249 GCAACAGGGTATTCGCCAAATACCCAGAAGACATAGCAGATTATTTCAAGCAGACATTTC 308

Qy   352 CTGAGGGGGTACTTCTGGGAACGAAGCAAGCATGACATACGAAGACCAGGGCATTGCATCGCCA 411
             |||||||||
Db   309 CTGAGGGGGTACTTCTGGGAACGAAGCAAGCATGACATACGAAGACCAGGGCATTGCATCGCCA 368

Qy   412 CAAACGACATAACAATGATGAAGAGGCGTCGACGACTGTTTTGCCTATAAAATTCGATTTG 471
             |||||||||
Db   369 CAAACGACATAACAATGATGAAGAGGCGTCGACGACTGTTTTGTCTATAAAATTCGATTTG 428

Qy   472 ATGGTGTGAACTTTCCTGCCAATGTCCAGTTATGCGCAGAGGAAGACGCTGAAATGGGAGC 531
             |||||||::
Db   429 ATGGTGTGAACTTTCCTGCCAATGTCCAGTTATGCGCAGAGGAAGACGCTGAAATGGGAGC 488

Qy   532 CATCCACTGAGATAATGTATGCGCGTGATGAGGTGCTGAAGGTGATGTTAACATGGCTC 591
             |||||||||
Db   489 CATCCACTGAGAAATGTATGCGCGTGATGAGGTGCTGAAGGTGATGTTAACATGGCTC 548

Qy   592 TGTTGCTTGAAGGAGGTGGCCATTACCGATGACTTCAAAACTACTTACAAAGCTAAGA 651
             |||:|||||
Db   549 TGTTGCTTGAAGGAGAGGTGGCCATTACCGACWTCAAAACTACTTACAGAGCTAAGA 608

Qy   652 AGGTTGTCCGGTTGCCAGACTATCACTTTGTGGACCATCGCATTGTGACGGCCACG 711
             |||||||||
Db   609 AGGTTGTCCGGTTGCCAGACTATCATTTTGTGGACCATCGCATTGTGAGCGCCACG 668

Qy   712 ACAAAGATTACAACAGGTTAAGCTGCACGAGCATGCCGAGCTCGTCATGGACTGTCAA 771
             |||||||||
Db   669 ACAAAGATTACAACAGGTTAAGCTGTATGAGCATGCCGAGCTCGTCATGGACTGTCAA 728

Qy   772 GGAAGGCCAAGTAAAGGCTTAATGAAAAGTCAAGACGACACGAGAGAAACAAAGTA-C 830
             |||||||||
Db   729 GGCGCGGCCAAGTAAAGGCTTAATGAAAAGTCAAGACGACACGAGAGAAACAAAGTATT 788

Qy   831 TTTTTGTTAAATTTGAAGGAATTTACTCGGAATTTCGATTCAAGG 890
             |||||||||
Db   789 TTTTTGTTAAATTTCAAGGAATTTACTCGGAATTTCGATTCAAGG 848

Qy   891 ATTTGTTCCGGGATTTGTTAGAGACTAGCTCTAGATTTGTATTGTTGTGAAAAA 944
             |||||||||
Db   849 ATTTGTTCCGGGACTTGTTAGAGACCAGCTCTAGAGTTTGTATTTGTGAAAAA 902

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RESULT 7
AF401282
LOCUS       AF401282               1046 bp    mRNA    linear    INV 05-AUG-2001
DEFINITION  Montastraea faveolata green fluorescent protein mRNA, complete cds.
ACCESSION   AF401282
VERSION     AF401282.1  GI:15081471
KEYWORDS    .
SOURCE      Montastraea faveolata
  ORGANISM  Montastraea faveolata
            Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Scleractinia;
            Faviina; Faviidae; Montastraea.
REFERENCE   1 (bases 1 to 1046)
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ORIGIN

Query Match   63.9%;   Score 681.2;   DB 11;   Length 729;
Best Local Similarity 98.1%;   Pred. No. 7.8e-181;
Matches 689;   Conservative 0;   Mismatches 13;   Indels 0;   Gaps 0;

```
Qy     81 ATGACAAGTGTTGCACAGGAAAAGGTGTGATTAAACCAGACATGAAGATGAAGCTGCGT 140
          ||||| |||||||||||||||||||||||||||||    || |||||||||||||||||
Db      1 ATGACCAGTGTTGCACAGGAAAAGGTGTGATTAAAAAAGAGATGAAGATGAAGCTGCGT 60

Qy    141 ATGGAAGGTGCTGTAAACGGGCACAAGTTCGTGGTTGAGGGAGATGGAAAAGGGAAGCCT 200
          |||||||||||||||||||||||||||||||||   | | ||||||||||| |||||||
Db     61 ATGGAAGGTGCTGTAAACGGGCACAAGTTCGTGATTCAAGGAGATGGAAATGGGAAGCCT 120

Qy    201 TTCGACGGAACACAGACTATGGATCATAGAGGCAACACAGGGCCACCATGCCTTTCGCT 260
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TTCGACGGAACACAGACTATGGATCATAGAGGCAACACAGGGCCACCATGCCTTTCGCT 180

Qy    261 TACGATATCTTGACAACAGTATTCGATTACGGCAACAGGGTATTCGCCAAATACCCAGAA 320
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TACGATATCTTGACAACAGTATTCGATTACGGCAACAGGGTATTCGCCAAATACCCAGAA 240

Qy    321 GACATAGCAGATTATTTCAAGCAGACGTTTCCTGAGGGGTACTTCTGGGAACGAGCATG 380
          ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GACATACCAGATTATTTCAAGCAGACGTTTCCTGAGGGGTACTTCTGGGAACGAGCATG 300

Qy    381 ACATACGAAGACCAGGGCATTTGCATCGCCACAAACGACATAACAATGATGGAAGGCGTC 440
          |||||||||||||||||||||||||||||||||||||||||||||||||| ||| ||||
Db    301 ACATACGAAGACCAGGGCATTTGCATCGCCACAAACGACATAACAATGATGAAAGACGTC 360

Qy    441 GACGACTGTTTTGCCTATAAAATTCGATTTGATGGTGTGAACTTTCCTGCCAATGTCCA 500
          |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GACGACTGTTTTGTCTATAAAATTCGATTTGATGGTGTGAACTTTCCTGCCAATGTCCA 420

Qy    501 GTTATGCGAGAGGAAGACGCCTGAAATGGGAGCCATCGAAATGTATGCGCGTGAT 560
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GTTATGCGAGAGGAAGACGCCTGAAATGGGAGCCATCGAAATGTATGCGCGTGAT 480

Qy    561 GGAGTGCTGAAGGGTGATGTTAACATGGCTCTGTTGCTTGAAGGAGGTGGCCATTACCGA 620
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GGAGTGCTGAAGGGTGATGTTAACATGGCTCTGTTGCTTGAAGGAGGTGGCCATTACCGA 540

Qy    621 TGTGACTTCAAAACTACTTACAAAGCTAAGAAGGTTGTCCGGTTGCCAGACTATCACTTT 680
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 TGTGACTTCAAAACTACTTACAAAGCTAAGAAGGTTGTCCGGTTGCCAGACTATCACTTT 600

Qy    681 GTGGACCATCGCATTGAGATTGTGAGACACGACAAGATTACAACAAGGTTAAGCTGCAC 740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GTGGACCATCGCATTGAGATTGTGAGACACGACAAGATTACAACAAGGTTAAGCTGCAC 660

Qy    741 GAGCATGCCGAAGCTCGTCGTCATGGACTCGTCAAGGAAGGCCAAG 782
          ||||||||||||||||||||||||||||||||||||||||||||||
Db    661 GAGCATGCCGAAGCTCGTCGTCATGGACTCGTCAAGGAAGGCCAAG 702
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Db    581 TGAAGGAGGTGGCCATTACCGATGTGACTTCAAAACTACATACAAAGCTAAGAGTTTGT 640
Qy    659 CCGGTTGCCAGACTATCACTTGTGCCAGACCATGCCATTGAGGATTGTGAGCCGACCAAAGA 718
          ||| ||||||||||||||||||  |||| |||||||||  ||||||||||||||||||||
Db    641 CCAGTGCCAGACTATCACTTGTGGACCATCGCCATTCGGGCTCGGGCTGCCGAGGCCAGGC 700

Qy    719 TTACAACAAGGTTAAGCTGCACGACATGCCGAAGCTCGTCGACGACTGTCAAGGAAGGC 778
          ||||||||||||||||||||   |||||||||||||| ||  |||||| |||||||||
Db    701 TTACAACAAGGTTAAGCTGTATGAGCATGCCGAAGCTCATTCTGGGCTGCCGAGGCCAGGC 760

Qy    779 CAAGTAAAGGCTTAATGAAAAGTCAAGACGACAACGAGGAGAAACAAGACTACTTTTTTGT 838
          |||||||||||||||  |||| | ||||||||||||  |||||| ||||| | ||||| |
Db    761 CAAGTAAAGGCTTAACAAAAGCCAAGACGACAACAAGGAGAAAAACAAGTGTCTCTT-T 819

Qy    839 TAAATTTGAAGGCATTTACTCGGAATTAGTATTTGATACTTCGATTCAAGGATTTGTTC 898
          |   ||||||| |||||||| |  |||||||||| |||||||| ||||||||||||||||
Db    820 TTTATTGAAAGGCATTTACTACTCAGAATTAGTATTTGGTACTTCAATTCAAGGATTTGTTT 879

Qy    899 CGGGATTTGTTGTAGAGACTAGCTCTAGAGTTGTATTTTGTGAAAAAAGA---TAGTTTTC 954
          ||||||||||||||||||||||||||  ||  ||| ||||||||||||||      |||||
Db    880 CGGGATTTGTTGTAGAGACTAGCTCTCGAGGGTTAAATTTTGTGAAAAAAGAGTTTTTTTCC 939

Qy    955 AGTTTTTCGGGGATTACAGCATGGGGATAGACTTTTTTAAACTCAGTTGTGGTCAAATGCA 1014
          | | |||||||||||||| ||| |||||||||||||| ||||||||||||||||||||||
Db    940 ATCTTTTCGGGGATTACAACATTAGGATAGACTTTTTAAACTCAGTTGTGGTCAAATGCA 999

Qy   1015 AGTAAGAAAACTGTAGTGAGAATAAACTTGTTATCGGAAGCCGAAAAAAAA 1063
          ||||  |||||||||||||||||||||||||||||||||||||||||||||
Db   1000 AGTA--AAAACTGTAGTGAGAATAAACTTGTTATCGGAAGCCGAAAAAAAA 1046
```

RESULT 8
AY182015
LOCUS   AY182015   729 bp   mRNA   linear   SYN 25-JUN-2003
DEFINITION Synthetic construct green fluorescent protein R3 mRNA, complete
            cds.
ACCESSION   AY182015
VERSION   AY182015.1 GI:32188185
KEYWORDS   synthetic construct
SOURCE   synthetic construct
  ORGANISM other sequences; artificial sequences.
REFERENCE   1 (bases 1 to 729)
  AUTHORS   Kelmanson,I.V. and Matz,M.V.
  TITLE   Molecular Basis and Evolutionary Origins of Color Diversity in
            Great Star Coral Montastraea cavernosa (Scleractinia: Faviida)
  JOURNAL   Mol. Biol. Evol. 20 (7), 1125-1133 (2003)
  PUBMED   12777529
REFERENCE   2 (bases 1 to 729)
  AUTHORS   Kelmanson,I.V. and Matz,M.V.
  TITLE   Direct Submission
  JOURNAL   Submitted (17-NOV-2002) Whitney Laboratory, University of Florida,
            9505 Ocean Shore Blvd, St Augustine, FL 32080, USA
FEATURES   Location/Qualifiers
     source   1..729
                     /organism="synthetic construct"
                     /mol_type="mRNA"
                     /db_xref="taxon:32630"
                     /note="designed for bacterial expression; derived from
                     Montastraea cavernosa (red morph)"
     CDS   1..729
                     /codon_start=1
                     /transl_table=11
                     /product="green fluorescent protein R3"
                     /protein_id="AAO64988.1"
                     /db_xref="GI:32188186"
                     /translation="MTSVAQEKGVIKKEMKMKLRMEGAVNGHKFVIQGDGIGKPFDGT
                     QTMDLTVIEGAPLPFAYDILTTVFDYGNRVFAKYPEDIPDYFKQTFPEGYFWERSMTY
                     EDQGICIATNDITMMKDVDDCFVYKIRFDGVNFPANGPVMQRKTLKWEPSTEIMYARD
                     GVLKGDVNMALLLEGGGHYRCDFKTTYKAKKVVQLPDYHFVDHRIEIVRHDKDYNKVK
                     LHEHAEARHGLSRKAKAHHHHHH"
     primer_bind   1..25
     primer_bind   complement(678..729)

RESULT 9
AY181552
LOCUS   AY181552   1045 bp   mRNA   linear   INV 25-JUN-2003
DEFINITION Montastraea cavernosa isolate mc1 red fluorescent protein mRNA,
            complete cds.
ACCESSION   AY181552
VERSION   AY181552.1 GI:32188165
KEYWORDS   .
SOURCE   Montastraea cavernosa (great star coral)
  ORGANISM Montastraea cavernosa
            Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Scleractinia;
            Faviina; Faviidae; Montastraea.
REFERENCE   1 (bases 1 to 1045)
  AUTHORS   Kelmanson,I.V. and Matz,M.V.
  TITLE   Molecular Basis and Evolutionary Origins of Color Diversity in
            Great Star Coral Montastraea cavernosa (Scleractinia: Faviida)
  JOURNAL   Mol. Biol. Evol. 20 (7), 1125-1133 (2003)
  PUBMED   12777529

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Db   632 GTGTCAAGTTACCAGATTATCACTTTGTGATCACTCCATTGAGATTTTGCGCCATGACA 691
Qy   715 AAGATTACAACAAGGTTAAGCTGCACGAGCATGCGAGCTCGTCATGGACTCGTCAAGGA 774
            |||| |||  ||||||||||||| ||| |||||||||||||||  || ||| || |||
Db   692 AAGAATACACTGAGGTTAAGCTGTATGAGCATGCGAGCTCATTCTCGGCGTCGCCGAGGG 751

Qy   775 AGGCAAGTAAAGGCTTAATGAAAAGTCAAGACGACAACGAGGAGAAACAAAGTACTTTT 834
            |||||||| |||||||||| ||||| |||||| |||||  | ||||||||    |||||
Db   809 TGGCAAAGTAAAGGCTTAACGAAAAGCCAAGACCACAAAAGAGAGAAAAAA--ATTTCG 809

Qy   835 TTGTTAAATTTGAAGGCATTTACTCGGAATTAGTATTTGATACTTTCGATTCAAGGATTT 894
            |||  |  ||| |||||||||||  |||||||| | |||||| || |||||||| |||||
Db   810 TTTTTCTATTGAAAGGCCATTTACTCGGATTACTTTGATACTTTTGATTCAAGGTTTT 869

Qy   895 GTTCCGGGATTTGTTAGAGACTAGCTCTA------GAGTTGTATTTGTGAAAAAAGATA 948
            || |||||| | ||| |||||||||||||      |||| |||||| |||||| |||||
Db   870 GTTACGGGACTTGTTGGAGACTAGCTCTCAACAACTAGCTAATGAAGTTTGTGGAAAAAG 929

Qy   949 GTTTCCAGTTTTCGGGATTACAGCAGCATGGGGATAGACTTTTAAACTCAGTTGTGGTCA 1008
            ||| |||| ||||  | |||| ||| |||| |  |||||  || ||  |||||||||  |
Db   930 TTTTCCAATTTTTCTGGATTACCATAAGGATAAGGATAGATTCTTTAAACTCAGTTGTGGAA 989

Qy  1009 AATGCAAGTAAGAAAAACTGTAGTGAGAATAAACTTGTTATCGGAAGCCGAAAAAAA 1064
            |||| |||||||||||||||  || ||||| ||| ||||  ||||| |||| ||||||
Db   990 AATACAAGTAAGAAAAATATAGTGAGAATAAATTTGTTGTGTCGGAAGCCAGAAAAAA 1045


RESULT 10
AY181553
LOCUS       AY181553                  836 bp    mRNA    linear    INV 25-JUN-2003
DEFINITION  Montastraea cavernosa isolate mc2 green fluorescent protein mRNA,
            complete cds.
ACCESSION   AY181553
VERSION     AY181553.1  GI:32188167
KEYWORDS    .
SOURCE      Montastraea cavernosa (great star coral)
  ORGANISM  Montastraea cavernosa
            Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Scleractinia;
            Faviina; Faviidae; Montastraea.
REFERENCE   1  (bases 1 to 836)
  AUTHORS   Kelmanson,I.V. and Matz,M.V.
  TITLE     Molecular Basis and Evolutionary Origins of Color Diversity in
            Great Star Coral Montastraea cavernosa (Scleractinia: Faviida)
  JOURNAL   Mol. Biol. Evol. 20 (7), 1125-1133 (2003)
  PUBMED    12777529
REFERENCE   2  (bases 1 to 836)
  AUTHORS   Kelmanson,I.V. and Matz,M.V.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-NOV-2002) Whitney Laboratory, University of Florida,
            9505 Ocean Shore Blvd, St Augustine, FL 32080, USA
FEATURES             Location/Qualifiers
     source          1..836
                     /organism="Montastraea cavernosa"
                     /mol_type="mRNA"
                     /isolate="mc2"
                     /db_xref="taxon:63558"
     CDS             84..767
                     /codon_start=1
                     /product="green fluorescent protein"
                     /protein_id="AAO61599.1"
                     /db_xref="GI:32188168"
                     /translation="MSVIKPDMKIKLRMEGAVNGHKFVIEGDGKGKPFEGTQSMDLTV
                     KEGAPLPFAYDILTTVFDYGNRVFAKYPQDIPDYFKQFFPEGYSWERSMTYEDGGICV
                     ATNDITLMKGVDDCFVYKIRFDGVNFPANGPVMQKKTLKWEPSTEKMYRDGVLKGDV
                     NMALLEGGHYRCDFKTTYKAKKFVQLPDYHFVDHRIBILSHDKDYNKVKLYEHAEAHS
                     HSGLPRQAK"
ORIGIN

Query Match          63.6%;  Score 678.4;  DB 2;  Length 836;
Best Local Similarity  89.5%;  Pred. No. 4.9e-180;
Matches  761;  Conservative  0;  Mismatches  66;  Indels  23;  Gaps  2;

Qy     1 ATTCGCCCCTGGTGATTGGAAGAGAGCAGATCGAGAACAACAAGAGCTG--TAAGGTTGA 58
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AUTHORS   Matz,M.V. and Lukyanov,S.A.
TITLE   Diversity and evolution of GFP-like fluorescent proteins
JOURNAL   Unpublished
REFERENCE 2 (bases 1 to 1133)
AUTHORS   Matz,M.V. and Lukyanov,S.A.
TITLE   Direct Submission
JOURNAL   Submitted (30-MAY-2001) Institute of Bioorganic Chemistry RAS,
           Miklukho-Maklaya 16/10, Moscow 117871, Russia
FEATURES   Location/Qualifiers
     source   1..1133
                     /organism="Montastraea annularis"
                     /mol_type="mRNA"
                     /db_xref="taxon:48500"
     CDS   181..855
                     /note="FPmann"
                     /codon_start=1
                     /product="green fluorescent protein-like protein"
                     /protein_id="AAK71332.1"
                     /db_xref="GI:21303776"
                     /translation="MSMIKPEMKIKMRMDGAVNGHKFVITGEGSGEPPEGKQTMNLTV
                     IDGGPLPFAFDILTTAFDYGKRVFAKYPEDIPDYFKQSFPEGFSWERSMTYEDGGICI
                     ATNDIKMEGDCFSYEIRFDGVNFPANSPVMQKTVKWEPCTYEMYVRDGVLKGGLNMA
                     LLEGGGHFRCDLKTTYKAKKVVQMPDYHFVNHRLEITWHDEDYNNVKLSEHAEAHSG
                     LPRQAK"

ORIGIN
Query Match   62.4%;   Score 665; DB 2; Length 1133;
Best Local Similarity   80.4%;   Pred. No. 3.1e-176;
Matches 855; Conservative 2; Mismatches 162;   Indels 44;   Gaps 5;

Qy   1 ATTCGCCCTGGTGATTTGGAAGAGAGCAGATCGAGAACAACAGAGCTGTA--AGGTTGA 58
         ||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db   99 ATTCACCCTGGTGATTTGGAAGAGAGCAGATCGAGAACAACACCAAGAGCTGTATTACGCTAA 158

Qy   59 TATCTTACTTACGTCTACCATCATCATGACAAGTTGTGCACAGGAAAAGGGTGTGATTAAACC 118
         |||||||||||||||||||||||| ||||||||||||||||||
Db   62 TATCTTACTTACGTCTACCGTCATGA--------GTGTGATAAAACC 100

Qy   59 TATCTTACTTACGTCTACCATCATCATGACAAGTTGTGCACAGGAAAAGGGTGTGATTAAACC 118
         ||||||||||||||||||||||||||| ||||||
Db   159 AATCTTTACTTGCCTCTACCACCATGA------------GTATGATTAAACC 197

Qy   119 AGACATGAAGATGAAGCTGCGTATGGAAGGTGCTGTAAACGGGCACAAGTTCGTGGTTGA 178
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   198 AGAAATGAAGATCAAGATGCGTATGGACGGTGCTGTAAACGGGCACAAGTTCGTGATTAC 257

Qy   179 AGGAGATGGAAAAGGGAAGCCCTTCGACGGAACCAGACTATGGACCTTACAGTCATCATAGA 238
         ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   258 AGGGGAAGGAAGCGGCGAGCCTTTCGAGGGAAAAACAGACTATGGACCTTGACAGTCATAGA 317

Qy   239 AGGCGCACCATTGCCTTCGCTTACGATATTCTGACAACAGTATTCGATTACGGCAACAG 298
         |||||||||||||||||||||||||||||||||||||||||:|||||||||||||||||
Db   318 CGGCGGACCTCTGCCTTTCGCTTTCGACATCTTGACAACAGTATTCGATTACGGCCAMCAG 377

Qy   299 GGTATTCGCCAAATACCCAGAAGACATAGCAGATTATTCAAGCAGACGTTTCCTGAGGG 358
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   378 GGTATTCGCCAAATACCCAGAAGACATCCCAGACTATTTCAAGCAGTCGTTTCCTGAGGG 437

Qy   359 GTACTTCTGGGAACGAAGCATGACATACGAAGACACCAGGCATTGCATCCGCCACAAACGA 418
         |||:| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   438 GTTTTCTTGGGAGAGAAGCATGACGTACGAAGAGCGGGGGCATTTGCATCCGCCACAAATGA 497

Qy   419 CATAACAATGATGGAAGGCGTCGACGACTGTTTTGCCTATAAAATTCGATTTGATGGGTGT 478
         |||||||||| ||||||||||||||||||||||||||||||||||||||||
Db   498 CATAAAAATG--------GAAGGGGACTGCTTTTCCTATGAAATTCGATTTGATGGGGGT 548

Qy   479 GAACTTTCTGCCAATGTCCAGTTATGCAGAGGAAGACGCTGAAATGGGAGCGCTGAGCCATCCAC 538
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   549 GAACTTTCCTGCCAATGTCCAGTTATGCAGAAGAACCGTGAAATGGGAGCCATGCAC 608

Qy   539 TGAGATAATGTATGCGCGTGAGTTGCTGAAGGGTGCTGAAGGGTGATGTTAACATGGCTCGTTGCT 598
         ||:||| ||||||||||||||||||||||||||||||||||||||||
Db   609 TGRGGAAATGTATGTGCGTGATGGAGTGGTCTTAAAGGGTCTTAACATGGCTCGTTGCT 668

Qy   599 TGAAGGAGGTGGCCATTACCGATGTGACTTCAAAACTACTTACAAAGCTAAGAAGGTTGT 658
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   669 TGAAGGAGGTGGCCATTTCCGATGTGACTTCAAAACTACTTACAAAGCTAAGAAGGTTGT 728

ATSDIKMEGDCFIYEIQFHIGVNFPPNGPVMQKTLKWEPSTEKMYVRDGVLKGDVNMA
LLEGGGHYRCDFPRSTYKAKKVQLPDVHFVDHRIEILSHDNDYNTVKLSEDARARYS
MLPSQAK"

ORIGIN

Query Match   58.7%; Score 625.4; DB 2; Length 1046;
Best Local Similarity 80.2%; Pred. No. 4.7e-165;
Matches 875; Conservative 0; Mismatches 141; Indels 75; Gaps 9;

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Qy        1 ATTCGCCCTGGTGATTGGAAGAGAGCAGATCGAGAACAACAAGAGCTG--TAAGGTTGA 58
            ||||||||||||||||||||||||||||||||||||||||||||||||  ||||||||||
Db        2 ATTCGCCCTGGTGATTGGAAGAGAGCAGATCGAGAACAACAAGAGCTGTATAAGGTTGA 61

Qy       59 TATCTTACT----TACGTCTACCATCATGACAACAGTGTTGCACAGAAAAGGGTGTGATT 113
            |||||||||    ||||||||||||||||||||||                ||||||||||
Db       62 TACTGATCTTAGTATACGTCTACCATCATGA-----------------------GTGTGATT 100

Qy      114 AAACCAGACATGAAGATGAAGCTGCCTATGAGAGGTGCTGTAAACGGGCACACAGTTCGTG 173
            ||||| ||||||||||||||||||||||||||||||||||||  |||||||||||||||||
Db      101 AAACCAATCATGGAGATCAAGCTGCCTATGAGAGGTGCTGTAAACGGGCACACAAGTTCGTG 160

Qy      174 GTTGAAGGAGATGGAAAAGGAAGCCTTTCCACGGAACACAGACATGGACCTTACAGTC 233
            |||||| ||||||||||||||||||||||||||||||||||           |||||||
Db      161 ATTAAAGGAGAAGGAGAGGCCAAGCCTTCGAGGAACGACGAGACTATAAACCTTACAGTC 220

Qy      234 ATAGAAGGGCGCACCATTGCCTTTCGCTTACGATATCTTGACAACAGTATTCGATTACGGC 293
            |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db      221 AAAGAAGGGCGCACCTCTCCCTTTGCTTACGATATCTGACATCTGACATCAGCATCCAGTATGGT 280

Qy      294 AACAGGGTATTCGCCAGAGACATCCAGAGACATACAGACGATATTCAAGCAGACGTTTCCT 353
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      281 AACAGGGTATTCACCAGAGACATCCAGAGACATACCAGACATATTCAAGCAGACGTTTCCT 340

Qy      354 GAGGGGTACTTCTGGGAACCAAGCATGACATGACATACGAGAAGGCATTGCATCGCCACA 413
            |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db      341 GAAGGGTATTCGTGGGAGCGAATCATGGCTTATGAAGACCAGAGTATTTGCACGCGCCACA 400

Qy      414 AACGACATAACAAATGATGGAAGGCGTCGACGACTGTTTGCCTATAAAATTCGATTGAT 473
            ||||||||||||||||||            |||||||||||||||||||||||||||||
Db      401 AGCGACATGAAAAATG--------GAAGGCGACTGTTTATCTACGAGAAATTCAATTCAT 451

Qy      474 GGTGTGAACTTCCTGCCAGTTATGCAGAGGAAGCAGCGCTGAAAATGGGAGCCA 533
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      452 GGTGTGAACTTTCCACCCAATGGTCCAGTTATGCAGAAGAAGACGCGTGAAAATGGGAGCCA 511

Qy      534 TCCACTGAGATAATGATGCGCGTGATGAGTGTCGAAGGGTGTCTGAACATGGCTCTG 593
            ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db      512 TCCACTGAGAAAATGTATGTCGTGATGTCGTGATGAGTGTCGAAGGGTGATGTGAACATGGGCTCTG 571

Qy      594 TTGCTTGAAGGAGGTGGCCATTACCGATGTGACTTCAAAACTTACAAAGCTAAGAAG 653
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      572 TTGCTTGAAGGAGGTGGCCATTACCGATGTGACTTTCGAAGTACTTACAAAGCGAAGAAA 631

Qy      654 GTTGTCGCGGTTGCCAGATCATCACTTTGTGACCATCGCATTGAGATTGTGAGCCACGAC 713
            |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db      632 CGTGTTCAGTGCCAGATCATCACTTTGTGGACCATCACTTTTGAGATTTTGAGCCATGAC 691

Qy      714 AAAGATTACACAACAAGGTTAAGCTGCACGAGCAGCATGCCGAAGCTCG---TCATGGACTGTCA 770
            |||||||||||||||||||||||||||||||||||||||||||||||||   ||||||||||||
Db      692 AATGACTACAACACCGTAAAGCTGTCGAGGATGCCGAGGCTCCGCGTCCATTCTATGCTGCCG 751

Qy      771 AGGAAGGCAAGTAAAGGCTTAATGAAAAGTCAAGACAGACAACGAGGAGAAACAAA---- 826
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      752 AGTCAGGCCAAGTAAAGGCTTAACGAAAAGCTAAACAAGAAAAGCTAAACCAACAACAAGAGAAAAGTG 811

Qy      827 -------GTACTTTTTTTGTTAAATTTGAAGGCATTTACTCGGAAATTAGTATT 871
                   |||||||||||||||||||||||||||||||||||||||||||||||
Db      812 TTTTTAGTTTTTTTCTTTTCCTTTTTTTTTCTATTTAAAGGGAATTTAATGGTT 871

Qy      872 TGATACTTTCGATTCAAGGATTTGTTCCCGGGATTTTTAGACTAGCTCTAGAGTTGTA 931
            |||  ||||||||||||||||||||||||    |||||||||||||||||||||||||
Db      872 GAATA-TTTCGATCCAGGGATTT-----GCGATTTGTTAGCACTAGCTCTAGAGTTAAA 925

Qy      659 CCGGTTGCTCAGACTATCACTTTGTGGACCATCGCCATTGAGATTGTGAGCCACGACAAAGA 718
            |||||||||||||||||||||||||||||||||| ||  |||||||||||||||||||||||
Db      729 CCAGATGCCAGACTATCACTTTGTGAATCACCGACTGAGATTGAGATGTGAGCAGCAGGA 788

Qy      719 TTACACAACAAGGTTAAGCTGCACGAGCAGCCTGAAGCTTCGTCATGGACTGTCAAGGAAGGC 778
            |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db      789 TTTACAACAATGTTAAGCTGTCTGAGAATCATGGCATGCCGACTGCCAAGGCAGGC 848

Qy      779 CAAGTAAAGGCTTAATGAAAGTCAAGACGACAACAGAGGAGAAACA--------AAGTA 829
            ||||||||||||||||||||| ||||||||||| ||||||||||||        ||
Db      849 CAAATAAAGGCTTGACGAAAACGGCAAAGTACAAGAGAAAGATATATATATATAAATG 908

Qy      830 CTTTTTGTTAAATTTGAAGGCATTTACTTCGGAATGTATTTGATTTCAAG 889
            ||||| ||  ||||||||||||||  ||||||||||    ||||||||||
Db      909 TATATTTTTCAACTGAACTTTTGGATTTATTTGATTATGTTAGATTTCAATTCAAG 968

Qy      890 GATTTGTTCCCGGGATTTGTTGTAGAGACTAGCTCTAGAGTTGTTGTATTTTGTGAAAAAAGATAG 949
            ||||| ||||||||||||||| |||||||||||||||||||||||||||||| ||||||||
Db      969 GATTTATTTTGGGATTTTGCTAGCCACTAGCTTATTGTTAAATTAAGTTAAAGACG---G 1025

Qy      950 TTTCCAGTTTTTGCGGGATTACAGCATGGGGATAGACTTTTAAACTCAGTTGTGTCAA 1009
            |||||| ||||||||||||||||||  |||||||||    ||||||||||| ||||||
Db     1026 TTTAGCATTTTTTCGGTATTACAACAACATAGGCACAGACACGACGTCTTAACCCCAGTAGTGTGTCAG 1085

Qy     1010 ATGCAAGTAAGAAAACTGTAGTGAGAATAAACTTGTTATGAA 1052
            |||||| |||||| |||||| ||||||||||| |||||||||
Db     1086 GTACAAGTAAGAAAACTTGGTGAGAATAGACTTGTAGTCGAA 1128
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RESULT 12
AF384683
LOCUS   AF384683   1046 bp   mRNA   linear   INV 27-AUG-2001
DEFINITION   Montastraea cavernosa green fluorescent protein mRNA, complete cds.
ACCESSION   AF384683
VERSION   AF384683.2 GI:15298095
KEYWORDS   .
SOURCE   Montastraea cavernosa (great star coral)
  ORGANISM   Montastraea cavernosa
               Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Scleractinia;
               Faviina; Faviidae; Montastraea.
REFERENCE   1 (bases 1 to 1046)
  AUTHORS   Lesser,M.P., Barry,T.M., Mazel,C., Matz,M.V., Lukyanov,S.A.,
               Falkowski,P., Gorbunov,M. and Kolber,Z.
  TITLE   Green fluorescent proteins in Caribbean scleractinian corals
  JOURNAL   Unpublished
REFERENCE   2 (bases 1 to 1046)
  AUTHORS   Lesser,M.P. and Barry,T.M.
  TITLE   Direct Submission
  JOURNAL   Submitted (21-MAY-2001) Department of Zoology and Center for Marine
               Biology, University of New Hampshire, 46 College Road, Durham, NH
               03824, USA
REFERENCE   3 (bases 1 to 1046)
  AUTHORS   Lesser,M.P. and Barry,T.M.
  TITLE   Direct Submission
  JOURNAL   Submitted (27-AUG-2001) Department of Zoology and Center for Marine
               Biology, University of New Hampshire, 46 College Road, Durham, NH
               03824, USA
REMARK   Sequence update by submitter
COMMENT   On Aug 27, 2001 this sequence version replaced gi:14485239.
FEATURES   Location/Qualifiers
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     CDS   89..766
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                     /codon_start=1
                     /product="green fluorescent protein"
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                     /db_xref="GI:15298096"
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                     KEGAPLPFAYDILTSAFQYGNRVFTKYPDDIPDYFKQTPEGYSWERIMAYEDGSICT

Qy 932 TTTTGTGAAAAAGATAGTTTCCAGTTTTTGCGGGATTACAGCAGTGGGATAGAGACTTTTT 991
         ||| ||||||| | |||||| |||||| || | ||||||||
Db 926 GTTTATGATGAAAAAAGTTT----------CGGGATTCCATCACAAGAATAGAGACTTTTT 975

Qy 992 AAACTCAGTTGTGTGTCAAATGCAAGTAAGAAAACTGTAGTGAGAATAAACTTGTTATCGA 1051
         |||||||| |||||||||||||||||||||||||| ||||||||||||||||||||||||
Db 976 AAACTCAGTTGTAGACAAAAACAAGTAAGAAAACTTAAGTGAGAATAAACTTGTTATCCGA 1035

Qy 1052 AGCCGAAAAAA 1062
          ||||||||||
Db 1036 AGCCGAAAAAA 1046

RESULT 13
AY679112
LOCUS   AY679112   684 bp   mRNA   linear   INV 25-AUG-2004
DEFINITION Montastraea faveolata green fluorescent protein G1 mRNA, complete
            cds.
ACCESSION   AY679112
VERSION   AY679112.1 GI:51472056
KEYWORDS   .
SOURCE   Montastraea faveolata
  ORGANISM Montastraea faveolata
            Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Scleractinia;
            Faviina; Faviidae; Montastraea.
REFERENCE   1 (bases 1 to 684)
  AUTHORS   Carter,R.W., Gibbs,P.D.L. and Schmale,M.C.
  TITLE   Cloning of Cnidarian Fluorescent Protein Genes
  JOURNAL   Unpublished
REFERENCE   2 (bases 1 to 684)
  AUTHORS   Carter,R.W., Gibbs,P.D.L. and Schmale,M.C.
  TITLE   Direct Submission
  JOURNAL   Submitted (06-JUL-2004) MBF, University of Miami, 4600 Rickenbacker
            Cswy, Miami, FL 33129, USA
FEATURES   Location/Qualifiers
     source   1..684
                     /organism="Montastraea faveolata"
                     /mol_type="mRNA"
                     /db_xref="taxon:48498"
     CDS   1..684
                     /note="GFP-like; MfaG1"
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                     HSGLPRQAK"
ORIGIN
Query Match   58.6%; Score 624.8; DB 2; Length 684;
Best Local Similarity   94.6%; Pred. No. 6.6e-165;
Matches 647; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

Qy 102 AAGGGTGATGATTAAACCAGACAGAAGATGAAGATGAAGCGTATGAAGGTGCTGTAAACGGG 161
         || ||||||||||||||||||||||| |||||||||| |||||||||||||||||||||| *
Db   1 ATGAGTGTGATAAAACCAGATATGAAGATCAAGCTGCGTATGGAAGGTGCTGTAAACGGG 60

Qy 162 CACAAGTTCGTGTTGAAGGAGATGGAAAAGGAAGCCTTTCGACGGGACACAGACTATG 221
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Db   61 CACAAGTTCGTGATTGAAGGAGACGGAAAAGGCAAGCCTTTCGAGGGAAAAACAGACTATG 120

Qy 222 GACCTTACAGTCATAGAGAGGCCACCATTGCCTTCGCTTACGATATCTTGACAACAGTA 281
         |||||||||||||||||||||||| |||| ||||||| ||||| ||||| || ||||||||
Db 121 GACCTTACAGTCATAGAGAGGCCACCTTTGCCGTTCGCTTACGATATCTTGACAACAGTT 180

Qy 282 TTCGATTACGGCAACAGGGTATTCGCCAAATACCCAGAAGACATAGCCAGATTATTCAAG 341
         ||||||||||| ||||||||||||||| |||||||| ||||||| ||| ||||||||||
Db 181 TTCGATTACGGCAACAGGGTATTCGCCAAATACCCAAAATACCCAAAATACCAGACTATTTCAAG 240

Qy 342 CAGACGTTCCTGAGGGGTACTTCTGGGAACGAAGCAGTGACACATACGAAGACCAGGCATT 401

FEATURES   Location/Qualifiers
     source   1..708
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ORIGIN

Query Match   58.3%;   Score 621.8; DB 11; Length 708;
Best Local Similarity   94.6%;
Matches 644;   Conservative   0;   Mismatches 37;   Indels   0;   Gaps   0;

Qy   102 AAGGGTGTGATTAAACCAGACATGAAGATGAAGATGCGTATGGAAGGTGCGTGTAAACGGG 161
                ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
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Qy   162 CACAAGTTCGTGGTTGAAGGAGATGAAAAGGAAGCCTTTGACGGAACACAGACTATG 221
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Qy   342 CAGACGTTTCCTGAGGGGTACTTCGCTTACGATGTGACTTCGCTTACGATATCTTGACAACAGTA 401
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Qy   402 TGCATCGCCACAAACGACATAACAATGATGAAGGCGTCGACGACTGTTTTGCCTATAAA 461
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Db   301 TGCATCGCCACGAACGACATAACAATGAAAGGCGTCGATGACTGTTTTCTCTATAAA 360

Qy   462 ATTCGATTTGATGGTGTGAACTTTCCTGCCAATGGTCCAGTTATGCAGAGGAAGACGCTG 521
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Db   601 CTGAGCCACGACAAAGATTACAACAAGGTTAAGCTGTATGAGCATGCCGAAGCTCATTCT 660

Qy   762 GGACTGTCAAGGAAGGCCAAG 782
                ||||||||||||||||||||
Db   661 GGGCTGCCGAGGGGTGCAAAG 681

Matches 646; Conservative   0; Mismatches 38; Indels   0; Gaps   0;

Qy   102 AAGGGTGTGATTAAACCAGACATGAAGATGAAGATGCGTATGGAAGGTGCGTGTAAACGGG 161
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Qy   342 CAGACGTTTCCTGAGGGGTACTTCGCTTACGATGTGACTTCGTCAT 401
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Qy   402 TGCATCGCCACAAACGACATAACAATGATGAAGGCGTCGACGACTGTTTTGCCTATAAA 461
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Qy   462 ATTCGATTTGATGGTGTGAACTTTCCTGCCAATGGTCCAGTTATGCAGAGGAAGACGCTA 521
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Qy   642 AAAGTAAGAAGGTTGTCCGGTTGCCAGACTCACTTTGTGGACCATCGCATTGAGATT 701
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Db   541 AAAGTAAGAAGGTTGTCCAGTTGCCAGACTCATCATTTTGTGGACCATCGCATTGAGATT 600

Qy   702 GTGAGCCACGACAAAGATTACAACAAGGTTAAGCTGCACACAAGCATGCCGAAGCTCGTCAT 761
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Qy   762 GGACTGTCAAGGAAGGCCAAGTAA 785
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RESULT 15
AY182016
LOCUS   AY182016   708 bp   mRNA   linear   SYN 25-JUN-2003
DEFINITION Synthetic construct green fluorescent protein R4 mRNA, complete
            cds.
ACCESSION   AY182016
VERSION   AY182016.1 GI:32188187
KEYWORDS   .
SOURCE   synthetic construct
  ORGANISM synthetic construct
            other sequences; artificial sequences.
REFERENCE   1 (bases 1 to 708)
  AUTHORS   Kelmanson,I.V. and Matz,M.V.
  TITLE   Molecular Basis and Evolutionary Origins of Color Diversity in
            Great Star Coral Montastraea cavernosa (Scleractinia: Favida).
  JOURNAL   Mol. Biol. Evol. 20 (7), 1125-1133 (2003)
  PUBMED   12777529
REFERENCE   2 (bases 1 to 708)
  AUTHORS   Kelmanson,I.V. and Matz,M.V.
  TITLE   Direct Submission
  JOURNAL   Submitted (17-NOV-2002) Whitney Laboratory, University of Florida,
            9505 Ocean Shore Blvd, St Augustine, FL 32080, USA

us-10-757-356-17.rge

Search completed: April 5, 2006, 21:46:56
Job time : 3834 secs

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                    GenCore version 5.1.7
          Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on:     April 5, 2006, 20:42:49 ; Search time 766 Seconds
                                      (without alignments)
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Title:           US-10-757-356-17
Perfect score:   1066
Sequence:        1 attcgccctggtgattgga.........atcgaagccgaaaaaaaaa 1066

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        496997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters:        9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Database :   N_Geneseq_21:*
         1: geneseqm1980s:*
         2: geneseqm1990s:*
         3: geneseqm2000s:*
         4: geneseqm2001aas:*
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        13: geneseqm2004bs:*
        14: geneseqm2005s:*

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1066	100.0	1066	8	AAL60081	Aal60081 Montastra
2	838.8	78.7	913	8	AAL60085	Aal60085 Montastra
3	665	62.4	1133	8	AAL60086	Aal60086 M. annula
4	628	58.9	684	-10	ADH00980	Adh00980 Montastra
5	628	58.9	684	12	ADO78073	Ado78073 M. cavern
6	628	58.9	684	14	ADZ84228	Adz84228 Montastra
7	626.4	58.8	684	12	ADO78071	Ado78071 M. cavern
8	626.4	58.8	684	14	ADZ84226	Adz84226 Montastra
9	540	50.7	684	14	ADW43033	Adw43033 Favia fav
10	540	50.7	684	14	ADW43022	Adw43022 Favia fav
11	536.8	50.4	684	14	ADW43035	Adw43035 Favia fav
12	533.6	50.1	684	14	ADW43041	Adw43041 Favia fav
13	533.4	50.0	795	8	AAL60080	Aal60080 Montastra
14	527.2	49.5	684	14	ADW43037	Adw43037 Favia fav
15	527.2	49.5	684	14	ADW43039	Adw43039 Favia fav
16	517.2	48.5	860	10	ABZ76493	Abz76493 M. cavern
17	507.4	47.6	729	14	ADY53076	Ady53076 Great sta
18	507.2	47.6	678	14	ADY53068	Ady53068 Great sta
19	499.2	46.8	681	13	ADU21136	Adu21136 M. cavern
20	497.8	46.7	729	14	ADY53077	Ady53077 Great sta
21	497.4	46.7	678	14	ADY53069	Ady53069 Great sta
22	486.4	45.6	678	10	ADD67209	Add67209 Galaxea f
23	467.2	43.8	675	14	ADY53067	Ady53067 Great sta
24	467.2	43.8	726	14	ADY53075	Ady53075 Great sta
25	465	43.6	726	10	ADH00962	Adh00962 Montastra
26	465	43.6	1111	6	ABK96463	Abk96463 cDNA frag
27	462	43.3	1113	6	ABK96462	Abk96462 cDNA frag
28	461.8	43.3	726	10	ADH00964	Adh00964 Montastra
29	460.2	43.2	726	10	ADH00972	Adh00972 Montastra
30	458.6	43.0	726	10	ADH00970	Adh00970 Montastra
31	457	42.9	726	10	ADH00968	Adh00968 Montastra
32	455.4	42.7	726	10	ADH00966	Adh00966 Montastra
33	436	40.9	745	10	ADH00976	Adh00976 Montastra
34	436	40.9	746	10	ADH00974	Adh00974 Montastra
35	435.2	40.8	675	14	ADW21090	Adw21090 Lobophytu
36	433	40.6	690	12	ADL72772	Adl72772 S. vitien
37	433	40.6	748	10	ADH00978	Adh00978 Montastra
38	432.8	40.6	684	10	ADN62702	Adn62702 Reporter
39	431.6	40.5	681	10	ADH00960	Adh00960 Montastra
40	430.2	40.4	678	12	ADL72766	Adl72766 T. geoffr
41	429.8	40.3	690	12	ADL72774	Adl72774 S. vitien
42	429.8	40.3	690	12	ADL72770	Adl72770 S. vitien
43	425.4	39.9	678	12	ADL72768	Adl72768 T. geoffr
44	421.2	39.5	1116	3	AAA52766	Aaa52766 Clavulari
45	421.2	39.5	1116	4	AAD03611	Aad03611 Clavulari

ALIGNMENTS

```
RESULT 1
AAL60081
ID   AAL60081 standard; DNA; 1066 BP.
XX
AC   AAL60081;
XX
DT   27-AUG-2003  (first entry)
XX
DE   Montastraea cavernosa green fluorescent protein (mcavGFP) encoding DNA.
XX
KW   Chromoprotein; fluorescent protein; colouring agent; food composition;
KW   cosmetic; fluorescence resonance energy transfer; calcium ion indicator;
KW   biosensor; pH indicator; phosphorylation indicator; messenger detector;
KW   transgenic animal; fluorescent timer; green fluorescent protein; GFP;
KW   transgenic; gene; ds.
XX
OS   Montastraea cavernosa.
XX
FH   Key             Location/Qualifiers
FT   CDS             81..785
FT                   /*tag= a
FT                   /product= "mcavGFP protein"
XX
PN   WO2003042401-A2.
XX
PD   22-MAY-2003.
XX
PF   12-NOV-2002; 2002WO-US036499.
XX
PR   13-NOV-2001; 2001US-0332980P.
XX
PA   (CLON-) CLONTECH LAB INC.
XX
PI   Labas YA, Gurskaya NG, Yanushevich Y, Fradkov AF, Lukyanov K;
PI   Lukyanov S, Matz MV;
XX
DR   WPI; 2003-482353/45.
DR   P-PSDB; AAO29586.
XX
PT   New chromo and/or fluorescent-protein encoding nucleic acids, the
PT   proteins being useful as labels in analyte detection assays, as
PT   selectable markers in recombinant DNA application, or as biosensors in
```

PT   prokaryotic and eukaryotic cells.
XX
PS   Claim 1; Fig 16; 88pp; English.
XX
CC   The invention relates to novel chromo and/or fluorescent proteins and
CC   nucleic acid molecules encoding such proteins. Sequences of the invention
CC   are useful as labelling tools for marking a protein, cell or organism in
CC   biochemistry, molecular biology and medical diagnostic applications.
CC   Chromoproteins are useful as colouring agents capable of imparting colour
CC   or pigment to a particular composition of matter, e.g. food compositions,
CC   pharmaceuticals or cosmetics, as labels in analyte detection assays, or
CC   as selectable markers in recombinant DNA applications. Fluorescent
CC   proteins are useful in fluorescence resonance energy transfer
CC   applications, in high-throughput screening assays, as biosensors in
CC   prokaryotic and eukaryotic cells e.g. as calcium ion indicator, as pH
CC   indicator or as phosphorylation indicator, as second messenger detectors,
CC   as in vivo markers in transgenic animals, or as fluorescent timers. The
CC   present sequence is Montastraea cavernosa green fluorescent protein
CC   (mcavGFP) encoding DNA
XX
SQ   Sequence 1066 BP; 336 A; 188 C; 272 G; 270 T; 0 U; 0 Other;

Query Match   100.0%; Score 1066; DB 8; Length 1066;
Best Local Similarity   100.0%;
Matches 1066; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 ATTCGCCCTGGTGATTTGGAAGAGAGCAGATCGAGAACAACAAGAGCTGTAAGGTTGATA 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATTCGCCCTGGTGATTTGGAAGAGAGCAGATCGAGAACAACAAGAGCTGTAAGGTTGATA 60

Qy   61 TCTTACTTACGTCTACCATCATGACAAGTGTTGCACAGGAAAAGGGTGTGATTAAACCAG 120
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Qy   121 ACATGAAGATGAAGCTGCGTATGGAAGGTGCTGTAAACGGGCCACAAGTTCGTGGTTGAAG 180
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Qy   181 GAGATGAAAAGGGAAGCCTTTCGACGGAACAACAGACTATGATGACCTTACGTCATCATAGAAG 240
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Db   181 GAGATGAAAAGGGAAGCCTTTCGACGGAACAACAGACTATGATGACCTTACGTCATCATAGAAG 240

Qy   241 GCGCACCATTGCCTTTCGCTTACGATATCTTGACAACAGTATTCGATTACGGCAACAGGG 300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 GCGCACCATTGCCTTTCGCTTACGATATCTTGACAACAGTATTCGATTACGGCAACAGGG 300

Qy   301 TATTCGCCAAATACCCAGAAGACATAGCAGATTATTCAAGCAGACGTTTCCTGAGGGGT 360
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Db   301 TATTCGCCAAATACCCAGAAGACATAGCAGATTATTCAAGCAGACGTTTCCTGAGGGGT 360

Qy   361 ACTTCTGGACAACGAAGCAATGACATGACGAAGACCAGGGCATTTGCATCGCCACAAACGACA 420
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Db   361 ACTTCTGGACAACGAAGCAATGACATGACGAAGACCAGGGCATTTGCATCGCCACAAACGACA 420

Qy   421 TAACAATGATGAAGGGGTCGACGACTTGTTTTGCCTATAAAATTCGATTCGATTGATGGTGTGA 480
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Db   421 TAACAATGATGAAGGGGTCGACGACTTGTTTTGCCTATAAAATTCGATTCGATTGATGGTGTGA 480

Qy   481 ACTTTCCTGCCAATGGTCCAGTTATGCAGAGAGAAGACGCTGAAATGGGAGGCCATCCACTG 540
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Db   481 ACTTTCCTGCCAATGGTCCAGTTATGCAGAGAGAAGACGCTGAAATGGGAGGCCATCCACTG 540

Qy   541 AGATAATGTATGCGCGTGAAGGGTGAGTGCTGAAGGGTGATGTTAACATGGCTTCTGTTGCTTG 600
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Db   541 AGATAATGTATGCGCGTGAAGGGTGAGTGCTGAAGGGTGATGTTAACATGGCTTCTGTTGCTTG 600

Qy   601 AAGGAGGTGGCCATTACCGATGTGACTTCAAAACTACTTACACAAGAGTTAAGAGAGGTTGTCC 660
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Qy   661 GGTTGCCAGACTATCACTTTGTGGACCATCGCATTGAGCCACCAGACCACCAAAGATT 720
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 GGTTGCCAGACTATCACTTTGTGGACCATCGCATTGAGCCACCAGACCACCAAAGATT 720

Qy   721 ACAACAAGGTTAAGCTGCACGAGCATGCCGAAGCTCGTCATGGACTGTCAAGGAAGGCCA 780
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Qy   781 AGTAAAGGCTTAATGAAAGTCAAGACGAGACACGAGGAGAACAAGTACTTTTTGTTA 840
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Db   781 AGTAAAGGCTTAATGAAAGTCAAGACGAGACACGAGGAGAACAAGTACTTTTTGTTA 840

Qy   841 AATTTGAAGGCATTTACTCGGAATTAGTATTGATACTTTCGATTCAAGGATTTGTTCCG 900
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Qy   901 GGATTTGTTAGAGACTAGCTCTAGAGTTGTATTTTGTGAAAAAAGATAGTTTCCAGTTT 960
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Qy   961 TGCGGGATTACAGCATGGGGATAGACTTTTTAAACTCAGTGTGGTCAAATGCAAGTAAG 1020
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RESULT 2
AAL60085
ID   AAL60085 standard; DNA; 913 BP.
XX
AC   AAL60085;
XX
DT   27-AUG-2003 (first entry)
XX
DE   Montastraea cavernosa green fluorescent protein (mcavGFP) 2 encoding DNA.
XX
KW   Chromoprotein; fluorescent protein; colouring agent; food composition;
KW   cosmetic; fluorescence resonance energy transfer; calcium ion indicator;
KW   biosensor; pH indicator; phosphorylation indicator; messenger detector;
KW   transgenic animal; fluorescent timer; green fluorescent protein; GFP;
KW   transgenic; gene; ds.
XX
OS   Montastraea cavernosa.
XX
FH   Key   Location/Qualifiers
FT   CDS   38..742
FT   /tag= a
FT   /product= "mcavGFP protein"
XX
PN   WO2003042401-A2.
XX
PD   22-MAY-2003.
XX
PF   12-NOV-2002; 2002WO-US036499.
XX
PR   13-NOV-2001; 2001US-0332980P.
XX
PA   (CLON-) CLONTECH LAB INC.
XX
PI   Labas YA, Gurskaya NG, Yanushevich Y, Fradkov AF, Lukyanov K,
PI   Lukyanov S, Matz MV;
XX
DR   WPI; 2003-482353/45.
DR   P-PSDB; AAO29590.
XX
PT   New chromo and/or fluorescent-protein encoding nucleic acids, the
PT   proteins being useful as labels in analyte detection assays, as
PT   selectable markers in recombinant DNA application, or as biosensors in
PT   prokaryotic and eukaryotic cells.
XX
PS   Claim 1; Fig 20; 88pp; English.
XX
CC   The invention relates to novel chromo and/or fluorescent proteins and

```
CC   nucleic acid molecules encoding such proteins. Sequences of the invention
CC   are useful as labelling tools for marking a protein, cell or organism in
CC   biochemistry, molecular biology and medical diagnostic applications.
CC   Chromoproteins are useful as colouring agents capable of imparting colour
CC   or pigment to a particular composition of matter, e.g. food compositions,
CC   pharmaceuticals or cosmetics, as labels in analyte detection assays, or
CC   as selectable markers in recombinant DNA applications. Fluorescent
CC   proteins are useful in high-throughput screening assays, as biosensors in
CC   prokaryotic and eukaryotic cells e.g. as calcium ion indicator, as pH
CC   indicator or as phosphorylation indicator, as second messenger detectors,
CC   as in vivo markers in transgenic animals, or as fluorescent timers. The
CC   present sequence is Montastraea cavernosa green fluorescent protein
CC   (mcavGFP) encoding DNA
XX
SQ   Sequence 913 BP; 279 A; 169 C; 231 G; 234 T; 0 U; 0 Other;

Query Match             78.7%;  Score 838.8;  DB 8;  Length 913;
Best Local Similarity   96.9%;  Pred. No. 6.1e-244;
Matches  866;  Conservative   0;  Mismatches  27;  Indels  1;  Gaps  1;

Qy         52 AGGTTGATATCTTACTTACGTCTACCATCATGACAAGTGTTGCACAGGAAAAGGGTGTGA 111
              ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db          9 AGGGTGATATCTTACTTACGTCTACCATCATGACAAGTGTTGCACAGGAAAAGGGTGTGA 68

Qy        112 TTAAACCAGACAATGAAGATGAAGCTGCGTATGGAAGGTGCTGTAAACGGGCACAAGTTCG 171
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         69 TTAAACCAGACAATGAAGATGAAGCTGCGTATGGAAGGTGCTGTAAACGGGCACAAGTTCG 128

Qy        172 TGGTTGAAGGAGATGAAAAGGGAGGCCTTTCGACGGAACACAGACTATGGACCTTACAG 231
              || |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        129 TGATTGAAGGAGATGAAAAGGGAGGCCTTTCGACGGAACACAGACTATGGACCTTACAG 188

Qy        232 TCATAGAAGGCGCACCATTGCCTTTCGCTTACGATATCTTGACAACAGTATTCGATTACG 291
              ||||||||| ||||||||||||||||||| |||||||||||||||||||||||||||||
Db        189 TCATAGAAGGGCACCATTGCCTTTCGCTATCTTGACAACAGTATTCGATTACG 248

Qy        292 GCAACAGGGTATTCGCCAAATACCCAGAAGACATAGCAGATTATTTCAAGCAGACGTTTC 351
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db        249 GCAACAGGGTATTCGCCAAATACCCAGAAGACATAGCAGATTATTTCAAGCAGACATTTC 308

Qy        352 CTGAGGGGTACTTCTGGGAACGAAGCATGACATGAGAAGGCAGGGCATTTGCATCGGCCA 411
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 CTGAGGGGTACTTCTGGGAACGAAGCATGACATGAGAAGGCAGGGCATTTGCATCGGCCA 368

Qy        412 CAAACGACATAACAATGATGGAAGGCGTCGACGACTGTTTTGCCTATAAAATTCGATTTG 471
              |||||||||||||||||||| |||||||||||||||||| ||||||||||||||||||
Db        369 CAAACGACATAACAATGATGAAAGGCGTCGACGACTGTTTTGTCTATAAAATTCGATTTG 428

Qy        472 ATGGTGTGAACTTTCCTGCCAATGTCCAGTTATGCAGAGGAAGACGCTGAAATGGGAGC 531
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        429 ATGGTGTGAACTTTCCTGCCAATGTCCAGTTATCGCAGAGGAAGACGCTGAAATGGGAGC 488

Qy        532 CATCCACTGAGATAATGTATGCGCGTGATGAGGTGCTGAAGGGTGATGTTAACATGGCTC 591
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        489 CATCCACTGAGATAATGTATGCGCGTGATGAGGTGCTGAAGGGTGATGTTAACATGGCTC 548

Qy        592 TGTTGCTTGAAGGAGGTGGCCATTACCGATGTGACTTCAAAACTACTTACAAAGCTAAGA 651
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db        549 TGTTGCTTGAAGGAGGTGGCCATTACCGATGTGACTTCAAAAACTACTTACACAGAGCTAAGA 608

Qy        652 AGGTTGTCCGGTTGCCAGACTATCACTTTGTGACCATCGCATTGAGATTGTGAGCCACG 711
              ||||||||| |||||||||||||| |||||||||||||||||||||||||||||||||
Db        609 AGGTTGTCCAGTTGCCAGACTATCATTTTGTGACCATCATCGCATTGAGATTGTGAGCCACG 668

Qy        712 ACAAAGATTACAACAAGGTTAAGCTGCACGAGCAGCATGCCGAAGCTCGTCATGACTGTCAA 771
              |||||||||||||||||||||||||| |||||||||||||||||||| ||| ||| | |
Db        669 ACAAAGATTACAACAAGGTTAAGCTGCATGAGCAGCATGCCGAAGCTCATTCTCGGGCTGCCGA 728

Qy        772 GGAAGGCCAAGTAAAGCTTAATGAAAAGTCAAGACGACAACAGGAGAAAACAAAGTA-C 830
              || ||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db        729 GGCAGGCCAAGTAAAGCTTAATGAAAAGTCAAGACGACAACAAGGAGAAAACAAAGTATT 788

Qy        831 TTTTTGTGTAAATTGAGGCATTACTCGGAATTAGTATTGATACTTCGATTCAAGG 890
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        789 TTTTTGTGTAAATTCAAGGCATTACTCGGAATTAGTATTGATACTTCGATTCAAGG 848

Qy        891 ATTTGTTCCGGATTGTTAGGACTAGCTCTAGAGTTGTATTTGTGAAAAAA 944
              |||||||| ||| ||||||| ||||||||||||||||||||| |||||||||
Db        849 ATTTGTTTCGGGACTTGTTAGAGACCAGCTCTAGAGTTGTATTTTGTGAAAAAA 902


RESULT 3
AAL60086
ID   AAL60086 standard; DNA; 1133 BP.
XX
AC   AAL60086;
XX
DT   27-AUG-2003  (first entry)
XX
DE   M. annularis green fluorescent protein (mannGFP) homologue encoding DNA.
XX
KW   Chromoprotein; fluorescent protein; colouring agent; food composition;
KW   cosmetic; fluorescence resonance energy transfer; calcium ion indicator;
KW   biosensor; pH indicator; phosphorylation indicator; messenger detector;
KW   transgenic animal; fluorescent timer; green fluorescent protein; GFP;
KW   transgenic; gene; ds.
XX
OS   Montastraea annularis.
XX
FH   Key            Location/Qualifiers
FT   CDS            181..855
FT                  /*tag= a
FT                  /product= "mannGFP protein"
FT                  /transl_except= (pos:373..375, aa:Xaa)
FT                  /transl_except= (pos:610..612, aa:Xaa)
FT                  /note= "Xaa = any amino acid"
XX
PN   WO200304 2401-A2.
XX
PD   22-MAY-2003.
XX
PF   12-NOV-2002; 2002WO-US036499.
XX
PR   13-NOV-2001; 2001US-0332980P.
XX
PA   (CLON-) CLONTECH LAB INC.
XX
PI   Labas YA, Gurskaya NG, Yanushevich Y, Fradkov AF, Lukyanov K;
PI   Lukyanov S, Matz MV;
XX
DR   WPI; 2003-482353/45.
DR   P-PSDB; AAO29591.
XX
PT   New chromo and/or fluorescent-protein encoding nucleic acids, the
PT   proteins being useful as labels in analyte detection assays, as
PT   selectable markers in recombinant DNA application, or as biosensors in
PT   prokaryotic and eukaryotic cells.
XX
PS   Claim 1; Fig 21; 88pp; English.
XX
CC   The invention relates to novel chromo and/or fluorescent proteins and
CC   nucleic acid molecules encoding such proteins. Sequences of the invention
CC   are useful as labelling tools for marking a protein, cell or organism in
CC   biochemistry, molecular biology and medical diagnostic applications.
CC   Chromoproteins are useful as colouring agents capable of imparting colour
CC   or pigment to a particular composition of matter, e.g. food compositions,
CC   pharmaceutical or cosmetics, as labels in analyte detection assays,
CC   as selectable markers in recombinant DNA applications. Fluorescent
CC   proteins are useful in fluorescence resonance energy transfer
CC   applications, in high-throughput screening assays, as biosensors in
CC   prokaryotic and eukaryotic cells e.g. as calcium ion indicator, as pH
CC   indicator or as phosphorylation indicator, as second messenger detectors,
CC   as in vivo markers in transgenic animals, or as fluorescent timers. The
CC   present sequence is Montastraea annularis green fluorescent protein
CC   (mannGFP) homologue encoding DNA
```

```
Db   1026 TTTAGCATTTTTCGGTATTACAACATAGGCACAGAGACGTCTTAACCCAGTAGTGGTCAG 1085
          || |||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Qy   1010 ATGCAAGTAAGAAAACTGTAGTGAGAATAAACTGTTATCGAA 1052
          || ||||||||||||| |||||||||||||||| ||||||||
Db   1086 GTACAAGTAAGAAAACTTGGTGAGAATAGACTTGTAGTCGAA 1128
```

RESULT 4
ADH00980
ID   ADH00980 standard; DNA; 684 BP.
XX
AC   ADH00980;
XX
DT   11-MAR-2004 (first entry)
XX
DE   Montastraea cavernosa green flourescent protein, Green II DNA.
XX
KW   Transcription regulation; biological study; drug screening;
KW   internal ribosome entry site; IRES;
KW   transcription-translation coupled system; green flourescent protein;
KW   Green II; gene; ds.
XX
OS   Montastraea cavernosa.
XX
FH   Key   Location/Qualifiers
FT   CDS   1..684
FT   /*tag= a
FT   /product= "Green II protein"
XX
PN   US2003157643-A1.
XX
PD   21-AUG-2003.
XX
PF   09-DEC-2002; 2002US-00314827.
XX
PR   24-AUG-2000; 2000US-00645706.
XX
PA   (ALMO/) ALMOND B D.
PA   (WOOD/) WOOD M G.
PA   (WOOD/) WOOD K V.
XX
PI   Almond BD, Wood MG,   Wood KV;
XX
DR   WPI; 2003-830146/77.
DR   P-PSDB; ADH00981.
XX
PT   Novel synthetic nucleic acid molecule from an aquatic species useful for
PT   imaging systems for in vivo biological studies or drug screening,
PT   comprises nucleotides of a coding region for a fluorescent polypeptide.
XX
PS   Disclosure; SEQ ID NO 21; 54pp; English.
XX
CC   The invention relates to a synthetic nucleic acid molecule comprising
CC   nucleotides of a coding region for a fluorescent polypeptide having a
CC   codon composition differing at more than 25% of codons from a parent
CC   nucleic acid sequence encoding a fluorescent polypeptide, where the
CC   nucleic acid has at least 3-fold fewer transcription regulatory sequences
CC   relative to average number of such sequences in the parent nucleic acid
CC   sequence. The invention is useful for in vivo biological studies or drug
CC   screening and is useful for detection of rare events that require extreme
CC   sensitivity (e.g. studying RNA encoding), in use with internal ribosome
CC   entry sites (IRES), to improve the efficiency of in vitro translation or
CC   in vitro transcription-translation coupled systems such as TNT (RTM)
CC   study of fluorescent proteins optimised to different host organisms (e.g.
CC   plants, fungi). The synthetic fluorescent proteins is used as reporters
CC   in multiwell assays and drug screening. The invention exhibits
CC   significantly enhanced levels of mammalian expression without negatively
CC   effecting other desirable physical or biochemical properties and has
CC   greatly reduced number of known transcription regulatory sequences. The
CC   present sequence is Montastraea cavernosa green flourescent protein,
CC   Green II DNA.
XX
SQ   Sequence 684 BP; 211 A; 137 C; 176 G; 160 T; 0 U; 0 Other;
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XX
SQ   Sequence 1133 BP; 344 A; 214 C; 277 G; 296 T; 0 U; 2 Other;

Query Match             62.4%;  Score 665;  DB 8;  Length 1133;
Best Local Similarity   80.4%;  Pred. No. 4.6e-191;
Matches  855;  Conservative    2;  Mismatches  162;  Indels   44;  Gaps    5;

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Qy      1 ATTCGCCCTGGTGATTTGGAAGAGAGCAGATCGAACAACAAGAGCTGTA--AGGTTGA 58
          ||||| |||||||||||||||||||||||||||||| ||||| ||||||||  ||||||
Db     99 ATTCACCCTGGTGATTTGGAAGAGAGCAGATCGAGAACAACCAAGAGCTGTATTACGCTAA 158

Qy     59 TATCTTACTTACGTCTACCATCATGACAAGTGTTGCACAGGAAAGGTGTGTGATTAAACC 118
          ||||||||||||    ||||||||||||          |||||||||||   ||||||||||
Db    159 AATCTTACTTACTTGCCTCTACCACCACCATGA----------GTATGATTAAACC 197

Qy    119 AGACATGAAGATGAAGCTGGGTATGGAAGGTGCTGTAAACGGGCACAAGTTCGTGGTTGA 178
          |||  ||||||| ||| ||| |||| | |||||  |||||||||||||||||||| ||  
Db    198 AGAAATGAAGATCAAGATGCGTATGCCGTGCTGTGTAAACGGGCACAAGTTCGTGATTAC 257

Qy    179 AGGAGATGAAAAGGGAGGAGCCTTTCGACGGAACAGACAGACCTTACAGTCATAGA 238
          |||  |  || ||| |||||||||||||  |||  ||||| |  || |||||||||
Db    258 AGGGGAAGGAAGCGGCGAGCCTTTCGAGGGAAAACAGACTATGCACCTGACAGTCATAGA 317

Qy    239 AGGCGCACCATTGCCCTTTCGCTTACGATATCTTGACAGTATTCGATTACGGCAACAG 298
          |||||  || |||||||| |||||  |||  ||||||| | ||||||||||||||| ||
Db    318 CGGCGGACCTCTGCCCTTCGCTTTCGCACATCTTGACACAGCATTCGATTACGGCACAG 377

Qy    299 GGTATTCGCCAAATACCCAGAAGACATAGCAGATTATTCAAGCAGACGTTCCTGAGGG 358
          ||||||||||||||||||||||||||||  |||| ||| ||||||| |||||||||||
Db    378 GGTATTCGCCAAATACCCAGAAGACATCCCAGACTATTTCAAGCAGTCGTTCCTGAGGG 437

Qy    359 GTACTTCTGGGAACGAAGCATGACATACGAAGACCAGGCCATTTGCATCGCCACAAACGA 418
          || |||| ||||||||||||||||  |||||||||  |||| |||||||||||||| |||
Db    438 GTTTTTCTTGGGAACGAAGCATGACTTACGAAGACGGGGCATTTGCATCGCCACAAATGA 497

Qy    419 CATAACAATGACATGATGAAGGCCGTCGACGACTTGTTTGCCTATAAAATTGATTGGTGT 478
          |||||  ||| |||||        ||||| | | ||||||  |||| |||| ||| | || 
Db    498 CATAAAAATG--------GAAGGCGACTGCTTTTCCTATGAAATTCGATTTGATGGGGT 548

Qy    479 GAACTTCCTGCCAATGGTCAGTTATGCAGAGGAAGACGCTGAAATGGGAGCCATCCAC 538
          |||||||||||||| |||| |||||||||| ||||||  |||||||||||||||| |||
Db    549 GAACTTCCTGCCAATAGTCCGTTATGCAGAGAAGAAGACCCGTGAAATGGGAGCCATGCAC 608

Qy    539 TGAGATAATGTATGCGCGTGATGGAGTGCTGAAGGGTGATGTTAACATGGCTCTGTTGCT 598
          || |  ||||||||||||||||||||||||||||| | | |  ||||||||||||||||||
Db    609 TGRGGAAATGTATGCGCGTGATGGAGTGCTGAAGGTGTGGTCTTAACATGGCTCTGTTGCT 668

Qy    599 TGGAGGAGTGGCCATTACCGATGGCGATTGGACTTCAAAACTACTTACAAAGAGAGGTTGT 658
          |||||||||||||||| ||||| ||| |||||||| ||||||||||||||||||||||||||
Db    669 TGGAGGAGTGGCCATTTCCGATGTGACTTGGACTTACAAAGTACTTACAAAGAGAGGTTGT 728

Qy    659 CCGGTTGCCAGACTATCACTTTGTGGACCATCGCATTGAGATTGTGAGCCACGACAAAGA 718
          || | ||||||||||||||||||||  ||||| || |||||| | ||  |  ||||||||
Db    729 CCAGATGCCAGACTATCACTTTGTGAATCATCACCGACTTGAGATAAACATGGCATGACGAGGA 788

Qy    719 TTACAACAAGGTTAAGCTGCCACGAGCATGCCGAGCTCGTCATGGACTGTCAAGGAGGC 778
          |||||||||  ||||||||| | |||||||||| ||| || || ||||| ||| | |||
Db    789 TTACAACAATGTTAAGCTGCTCGAGCATGCCGCAGCGTCCTCGACTGCCAAGCCAGCC 848

Qy    779 CAAGTAAAGGCTTAATGAAAAGTCAAGACGACAACGAGGAGAAACA------AAGTA 829
          ||| ||||||||| | ||||||  ||| | | ||| ||| |  |||      ||| 
Db    849 CAAATAAAGGCTTGACGAAAAGCCAAAAGCGGCAAAGAGTACAAGAAGTATATAAATG 908

Qy    830 CTTTTTGTAAATTGAAGGCATTACTCGGAATTAGTATTTCGATTCAAG 889
          | |||| | |||||||||||||  |||||||||||||||| |||||||
Db    909 TATATTTTCAACTGAAGGCATTCCACTCGGAATTAGTATTTCAATTCAAG 968

Qy    890 GATTGTTCCGGGATTGTTGTAGACTAGCTTCTAGAGTTGTATTTTGTGAAAAAGATAG 949
          |||| || ||||||| |||| | ||||||| | ||||| |||| || |||||||  | 
Db    969 GATTTATTTTGGGATTTTGCTAGCCACTAGCTTTATTGTTAATTAAGTTAAAGACG---G 1025

Qy    950 TTTCCAGTTTTTGCCGGATTACAGCATGGGGGATAGACTTTTTAAACTCAGTTGGTGGTCAA 1009
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Query Match          58.9%;  Score 628; DB 10; Length 684;
Best Local Similarity 94.9%;  Pred. No. 6.4e-180;
Matches 649; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

Qy    102 AAGGGTGTGATTAAACCAGACATGAAGATGAAGCTGCGTATGGAAGGTGCTGTAAACGGG 161
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Db      1 ATGAGTGTGATAAAACCAGACATGAAGATCAAGCTGCGTATGGAAGGTGCTGTAAACGGG 60

Qy    162 CACAAGTTCGTGTTGAAGGAGATGAGGAAAAAGGGAAGCCTTTCGACGGAACACAGACTATG 221
          ||||||||||||||||||| ||| |||| ||||||||||||||||||||||| |||||||
Db     61 CACAAGTTCGTGATTGAAGGAGACGGAAAAGGCGAAGCCTTTCGAGGGAAAAACAGACTATG 120

Qy    222 GACCTTACAGTCATAGAAGGGCCCACCATTGCCTTTGCTTACGATATCTTGACAACAGTA 281
          |||||||||||||||||||| |||||| ||||||||||||||||||||||||||||||||
Db    121 GACCTTACAGTCATAGAAGGGCCACCTTTGCCTTTGCTTACGATATCTTGACAACAGTA 180

Qy    282 TTCGATTACGGCAACAGGGTATTCGCCAAATACCCAGAAGACATAGCAGATTATTTCAAG 341
          |||||||||||||||||||||||||||||||||||||||||||||||| |||| |||||||
Db    181 TTCGATTACGGCAACAGGGTATTCGCCAAATACCCAGAAGACATACCAGACTATTTCAAG 240

Qy    342 CAGACGTTTCCTGAGGGGTACTTCTGGGAACGAAGCATGACATACGAAGACCAGGGCATT 401
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CAGACGTTTCCGGAGGGGTACTTCTGGGAACGAAGCATGACATACGAAGACCAGGGCATT 300

Qy    402 TGCATCGCCACAACGACATAACAATGATGAAAGGCGTCGACGACTGTTTTGCCTATAAA 461
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TGCATCGCCACAACGACATAACAATGATGAAAGGCGTCGACGACTGTTTTGTCTATAAA 360

Qy    462 ATTCGATTTGATGGTGTGAACTTTCCTGCCAATGTCCAGTTATGCGGAGGAAGGACGCTG 521
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ATTCGATTTGATGGTGTGAACTTTCCTGCCAATGTCCAGTTATGCAGAGGAAGGACGCTA 420

Qy    522 AAATGGGAGGCCATCCACTGAGATAATGTATGCGCGTGAGTCTGAAGGGTGATGTT 581
          |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db    421 AAATGGGAGGCCATCCACTGAGATAATGTATGCGCGTGAGTCTGAAGGGTGATGTT 480

Qy    582 AACATGGCTCTGTTGCTTGAAGGAGGTGGCCATTACCGATGTGACTTCAAAACTACTTAC 641
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 AACATGGCTCTGTTGCTTGAAGGAGGTGGCCATTACCGATGTGACTTCAAAACTACTTAC 540

Qy    642 AAAGCTAAGAAGGTTGTCCGGTTGCCAGACTATCACTTTTGTGGACCATCGCATTGAGATT 701
          ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db    541 AAAGCTAAGAAGGTTGTCCGGTTGCCAGACTATCATTTTGTTGACCATCGCATTGAGATT 600

Qy    702 GTGAGCCACGACAAAGATTACAACAAGTTAAGCTGCACGAGCATGCCGAAGCTGTCGTCAT 761
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db    601 GTGAGCCACGACAAAGATTACAACAAGTTAAGCTGTGTATGAGCCTGTATGAGCGAAGCTCATTCT 660

Qy    762 GGACTGTCAAGGAAGGCCAAGTAA 785
          |||||||||||||||||||||||||
Db    661 GGGCTGCCGAGGCAGGCCAAGTAA 684
```

RESULT 5
AD078073
```
ID   AD078073 standard; DNA; 684 BP.
XX
AC   AD078073;
XX
DT   26-AUG-2004 (first entry)
XX
DE   M. cavernosa green fluorescent protein mutant GreenII DNA.
XX
KW   fluorescent protein; red fluorescent protein; green fluorescent protein;
KW   gene expression detection; regeneration; multiple labeling system;
KW   in vivo marker; microinjection assay; taxonomic marker; colour indicator;
KW   food additive; cosmetic; gene; ds; mutant; GreenII; great star coral.
XX
OS   Montastraea cavernosa.
XX
FH   Key            Location/Qualifiers
FT   CDS            1..684
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FT                 /tag= a
FT                 /product= "M. cavernosa green fluorescent protein mutant
FT                 GreenII"
XX
PN   US2004110225-A1.
XX
PD   10-JUN-2004.
XX
PF   09-DEC-2002; 2002US-00314936.
XX
PR   09-DEC-2002; 2002US-00314936.
XX
PA   (GIBB/) GIBBS P D L.
PA   (CART/) CARTER R W.
PA   (SCHM/) SCHMALE M C.
XX
PI   Gibbs PDL, Carter RW, Schmale MC;
XX
DR   WPI; 2004-467659/44.
DR   P-PSDB; AD078074.
XX
PT   New first mutant fluorescent protein having an optical property
PT   relatively different to a corresponding optical property produced by a
PT   wild-type red or green fluorescent protein, useful for detecting
PT   expression of a gene.
XX
PS   Claim 33; SEQ ID NO 7; 30pp; English.
XX
CC   The invention describes a first mutant fluorescent protein (I) comprising
CC   an amino acid sequence that differs from that of a corresponding wild-
CC   type red fluorescent protein by an amino acid substitution, where the
CC   first mutation fluorescent protein mutant has an optical property that
CC   differs relative to the corresponding optical property produced by the
CC   wild-type red or green fluorescent protein. (I) is useful for detecting
CC   expression of gene. The polynucleotide (II) encoding (I) is useful for
CC   detecting expression of a gene which involves introducing (II) into a
CC   cell or organism, allowing the cell to replicate, and detecting
CC   expression of the nucleic acid by emission of fluorescent light. The
CC   expression of the nucleic acid expression is detected in vivo or in
CC   vitro. (II) is useful for regenerating an animal such as a zebrafish
CC   which contains (II). (I) is useful as a marker for detecting expression
CC   of a gene, in biochemical assays, and as reagents. (I) is also useful in
CC   multiple labeling systems, as in vivo markers such as in mRNA
CC   microinjection assays, and as taxonomic markers for studies of genetics,
CC   colour indicators in diagnostic kits, coloured food additives, and
CC   cosmetics ingredients. (I) is useful in research for up or down
CC   regulation, to monitor promoter activity, to allow longer term monitoring
CC   and to localise proteins. (I) has enhanced properties such as
CC   substantially enhanced fluorescence and reduced toxicity. This sequence
CC   encodes GreenII, a mutant of the wild type green fluorescent protein
CC   isolated from great star coral.
XX
SQ   Sequence 684 BP; 211 A; 137 C; 176 G; 160 T; 0 U; 0 Other;
```

```
Query Match          58.9%;  Score 628; DB 12; Length 684;
Best Local Similarity 94.9%;  Pred. No. 6.4e-180;
Matches 649; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

Qy    102 AAGGGTGTGATTAAACCAGACATGAAGATGAAGCTGCGTATGGAAGGTGCTGTAAACGGG 161
          |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGAGTGTGATAAAACCAGACATGAAGATCAAGCTGCGTATGGAAGGTGCTGTAAACGGG 60

Qy    162 CACAAGTTCGTGTTGAAGGAGATGAGGAAAAAGGGAAGCCTTTCGACGGAACACAGACTATG 221
          ||||||||||||||||||| ||| |||| |||||||||||||||||||||||| |||||||
Db     61 CACAAGTTCGTGATTGAAGGAGACGGAAAAGGCGAAGCCTTTCGAGGGAAAAACAGACTATG 120

Qy    222 GACCTTACAGTCATAGAAGGGCCCACCATTGCCTTTGCTTACGATATCTTGACAACAGTA 281
          |||||||||||||||||||| |||||| ||||||||||||||||||||||||||||||||
Db    121 GACCTTACAGTCATAGAAGGGCCACCTTTGCCTTTGCTTACGATATCTTGACAACAGTA 180

Qy    282 TTCGATTACGGCAACAGGGTATTCGCCAAATACCCAGAAGACATAGCAGATTATTTCAAG 341
          ||||||||||||||||||||||||||||||||||||||||||||||| |||| ||||||
Db    181 TTCGATTACGGCAACAGGGTATTCGCCAAATACCCAGAAGACATACCAGACTATTTCAAG 240
```

DR WPI; 2005-345399/35.
DR P-PSDB; AD284229.
XX
PT Novel mutant fluorescent protein comprising amino acid sequence that
PT differs from wild-type red or green fluorescent protein by amino acid
PT substitutions, useful as markers for detecting desired gene expression.
XX
PS Example 4, SEQ ID NO 7; 29pp; English.
XX
CC The invention relates to mutant red and green fluorescent proteins which
CC have higher fluorescent intensities compared to the wild-type proteins
CC from which they are derived. The invention also discloses nucleic acids
CC encoding the mutant fluorescent proteins, and transgenic animals
CC comprising such a nucleic acid. The mutant red fluorescent proteins (RFP)
CC of the invention, Red I (ADZ84223) and Red II (ADZ84225), are derived
CC from a novel wild-type RFP (referred to as Ac/DsRFP) isolated from a
CC mushroom coral believed to be either an Actinodiscus or Discosoma
CC species, while the mutant green fluorescent proteins (GFP), Green I
CC (AD284227) and Green (AD284229), are derived from a novel wild-type GFP
CC (known as McGFP) isolated from the great star coral Montastraea
CC cavernosa. The Ac/DsRFP and McGFP mutants were obtained by subjecting the
CC wild-type Ac/DsRFP and McGFP cDNAs to low-stringency PCR to introduce
CC random mutations, cloning the PCR products into bacterial expression
CC vectors, and selecting the transformed bacteria having higher relative
CC fluorescence compared to those expressing the wild-type proteins. The
CC mutant fluorescent proteins of the invention may be used in a wide range
CC of applications. They are useful as markers for detecting the expression
CC of a gene of interest, or can be used as in vivo markers in mRNA
CC microinjection assays in transgenic animals. They can be used in
CC expression systems (e.g., as components of fusion proteins), in multiple
CC labeling systems, or can be used in biochemical assays and as reagents.
CC They may additionally be used as taxonomic markers for studies of
CC cnidarian genetics, as color indicators in diagnostic kits, as colored
CC food additives and as cosmetic ingredients. The present sequence
CC represents DNA encoding the mutant Montastraea cavernosa green
CC fluorescent protein Green II. Green II, in contrast to the mutant GFP
CC Green I (AD284227), has a high resistance to photobleaching.
XX
SQ Sequence 684 BP; 211 A; 137 C; 176 G; 160 T; 0 U; 0 Other;

Query Match 58.9%; Score 628; DB 14; Length 684;
Best Local Similarity 94.9%; Pred. No. 6.4e-180;
Matches 649; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

```
Qy  102  AAGGGTGTGATTAAACCAGACATGAAGATGAAGCTGCGTATGGAAGGTGCTGTAAACGGG  161
              |||| |||| |||||||||||||||||||||||||||||||||||||||||||||
Db    1  ATGAGTGTGATAAAACCAGACATGAAGATGAAGCTGCGTATGGAAGGTGCTGTAAACGGG   60

Qy  162  CACAAGTTCGTGGTTGAAGGAGATGGAAAAGGAAGCCTTTGACGGAACACAGACTATG    221
         ||||||||||||| ||||||||| |||||| ||||||||||||||| |||||||||||
Db   61  CACAAGTTCGTGATTGAAGGAGACGGAAAAGGCAAGCCTTTGACGGAACACAGACTATG   120

Qy  222  GACCTTACAGTCATAGAGGGCGCACCATTGCCTTTCGCTTACGATATCTTGACAACAGTA  281
         |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db  121  GACCTTACAGTCATAGAGGGCGCACTTTGCCTTTCGCTTACGATATCTTGACAACAGTA   180

Qy  282  TTCGATTACGGCAACAGAGTATTCGCAACAACCAGAACATGACATACGAAGCAGAACATT  341
         |||||||||||||||||||||||||||||||||  ||||||  ||| |||
Db  181  TTCGATTACGGCAACAGAGTATTCGCAACAACCAAAAGAACATACCAGACTATTTCAAG   240

Qy  342  CAGACGTTCCTGAGGGGTACTTCTGGGAACGAAGCATGACATACGAAGCAGGGCATT     401
         |||||||| || |||||||||||  ||||||||||||||||||||  |||||||||
Db  241  CAGACGTTTCCGGAGGGGTACTTCCCGGGAACGAAGCATGACATGACCAGGGCATT      300

Qy  402  TGCATCGCCACAAACGACATAACAATGATGGAGGTCGACGACTGTTTTGCCTATAAA    461
         ||||||||||||||||||||||||| |||||  || |||||||||||||| ||||||
Db  301  TGCATCGCCACAAACGACATAACATGATGAAAGGCGTCGACGACTGTTTTGTCTATAAA  360

Qy  462  ATTCGATTTGATGGTGTGAACTTTCCTGCCAATGGTCAGTTATGCAGAGGAAGACGCTG   521
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361  ATTCGATTTGATGGTGTGAACTTTCCTGCCAATGGTCAGTTATGCAGAGGAAGACGCTA  420

Qy  522  AAATGGGAGCCATCCACTGAGATAATGTATGCGCCGTGATTGGAGTGCTGAAGGGTGATGTT  581
```

```
Qy  522  AAATGGGAGCCATCCACTGAGATAATGTATGCGCCGTGATTGGGGTACTGATGTT       581
         |||||||||||||||||||||||||||||||||||||||||||  ||||||||||
Db  421  AAATGGGAGCCATCCACTGAGATAATGTATGCGCCGTGATTGGGGTACTGATGTT       480

Qy  582  AACATGGCCTCGTTGCTTGCTTGAAGGAGGTGGCCATTACCGATGTGACTTCAAAACTACTTAC  641
Db  481  AACATGGCCTCGTTGCTTGCTTGAAGGAGGTGGCCATTACCGATGTGACTTCAAAACTACTTAC  540

Qy  642  AAAGTAAGAGGTTGTCCGTTGCCAGACTATCACTTTGTGGACCATCGCATTGAGATT     701
         |||||||||||||||||||||||||||||||| |||||| ||||||||||||||||
Db  541  AAAGTAAGAGGTTGTCCGTTGCCAGACTATCATTTTGTTGACCATCGCATTGAGATT     600

Qy  702  GTGAGCCACGACAAAGATTACAACAAGGTTAAGCTGCACGACATGCCGAAGCGTCGTCAT  761
         |||||||||||||||||||||||||||||||||||      ||||||||||| || ||
Db  601  GTGAGCCACGACAAAGATTACAACAAGGTTAAGCTGTATGAGCATGCCGAAGCTCATTCT  660

Qy  762  GGACTGTCAAGGAAGGCCAAGTAA  785
         || ||| |  ||| |||||||||
Db  661  GGGCTGCCGAGGCAGGCCAAGTAA  684
```

RESULT 6
AD284228
ID   AD284228 standard; DNA; 684 BP.
XX
AC   AD284228;
XX
DT   14-JUL-2005 (first entry)
XX
DE   Montastraea cavernosa GFP mutant Green II-encoding DNA, SEQ ID NO:7.
XX
KW   Green fluorescent protein; Green II; mutant; gene; ds.
XX
OS   Montastraea cavernosa.
OS   Synthetic.
XX
FH   Key   Location/Qualifiers
FT   CDS   1..684
FT   /tag= a
FT   /product= "Mutant GFP Green II"
FT   mutation replace(527,C)
FT   /tag= b
FT   /note= "This nucleotide is C in the Green I mutant,
FT   resulting in Ser rather than Phe at position 176 of the
FT   protein"
XX
PN   US2005100954-A1.
XX
PD   12-MAY-2005.
XX
PF   23-DEC-2004; 2004US-00021014.
PR   09-DEC-2002; 2002US-00314936.
XX
PA   (GIBB/) GIBBS P D L.
PA   (CART/) CARTER R W.
PA   (SCHM/) SCHMALE M C.
XX
PI   Gibbs PDL, Carter RW, Schmale MC;
XX

```
Db  421 |||||||||||||||||| |||||||||| | ||||||||||||
        AAATGGGAGCCATCCACTGAGATAATGTATGCGGGTGATGGAGTGGTGAAGGGTGATGTT 480
Qy  582 AACATGGCTCGTTGCTTGAAGGAGGTGGCCATTACCGATGTGACTTCAAAACTACTTAC 641
        |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db  481 AACATGGCTCGTTGCTTGAAGGAGGTGGCCATTACCGATGTGACTCCAAAACTACTTAC 540
Qy  642 AAAGCTAAGAAGGTTGTCCGGTTGCCGGTGCCAGACTATCACTTTGTGGACCATCCCATTGAGATT 701
        ||||||||||||||||||| |||||| ||||||||||| ||||| |||||||| |||||||||
Db  541 AAAGCTAAGAAGGTTGTCCAGTTGCCAGACTATCATTTTGTTGACCATCGCATTGAGATT 600
Qy  702 GTGAGCCACGACAAAGATTACACAAGGTTAAGCTGCCACGAGCATGCCGAAGCTCGTCAT 761
        |||||||||||||||||||||||||||||||||||  | |||||||||||||||||  |
Db  601 GTGAGCCACGACAAAGATTACACAAGGTTAAGCTGTATGAGCATGCCGAAGCTCATTCT 660
Qy  762 GGACTGTCAAGAAGGCCAAGTAA 785
        ||| || |||||||||||
Db  661 GGGCTGCCGAGGCAGGCCAAGTAA 684
```

RESULT 7
ADO78071
ID   ADO78071 standard; DNA; 684 BP.
XX
AC   ADO78071;
XX
DT   26-AUG-2004 (first entry)
XX
DE   M. cavernosa green fluorescent protein mutant GreenI DNA.
XX
KW   fluorescent protein; red fluorescent protein; green fluorescent protein;
KW   gene expression detection; regeneration; multiple labeling system;
KW   in vivo marker; microinjection assay; taxonomic marker; colour indicator;
KW   food additive; cosmetic; gene; ds; mutant; GreenI; great star coral.
XX
OS   Montastraea cavernosa.
XX
FH   Key   Location/Qualifiers
FT   CDS   1..684
FT   /tag= a
FT   /product= "M. cavernosa green fluorescent protein mutant
FT   GreenI"
XX
PN   US2004110225-A1.
XX
PD   10-JUN-2004.
XX
PF   09-DEC-2002; 2002US-00314936.
XX
PR   09-DEC-2002; 2002US-00314936.
XX
PA   (GIBB/) GIBBS P D L.
PA   (CART/) CARTER R W.
PA   (SCHM/) SCHMALE M C.
XX
PI   Gibbs PDL, Carter RW, Schmale MC;
XX
DR   WPI; 2004-467659/44.
DR   P-PSDB; ADO78072.
XX
PT   New first mutant fluorescent protein having an optical property
PT   relatively different to a corresponding optical property produced by a
PT   wild-type red or green fluorescent protein, useful for detecting
PT   expression of a gene.
XX
PS   Claim 32; SEQ ID NO 5; 30pp; English.
XX
CC   The invention describes a first mutant fluorescent protein (I) comprising
CC   an amino acid sequence that differs from that of a corresponding wild-
CC   type red fluorescent protein by an amino acid substitution, where the
CC   first mutation fluorescent protein mutant has an optical property that
CC   differs relative to the corresponding optical property produced by the
CC   wild-type red or green fluorescent protein. (I) is useful for detecting
CC   expression of gene. The polynucleotide (II) encoding (I) is useful for
CC   detecting expression of a gene which involves introducing (II) into a
CC   cell or organism, allowing the cell to replicate, and detecting
CC   expression of the nucleic acid by emission of fluorescent light. The
CC   expression of the nucleic acid expression is detected in vivo or in
CC   vitro. (II) is useful for regenerating an animal such as a zebrafish
CC   which contains (II). (I) is useful as a marker for detecting expression
CC   of a gene, in biochemical assays, and as reagents. (I) is also useful in
CC   multiple labeling systems, as in vivo markers such as in mRNA
CC   microinjection assays, and as taxonomic markers for studies of genetics,
CC   colour indicators in diagnostic kits, coloured food additives, and
CC   cosmetics ingredients. (I) is useful in research for up or down
CC   regulation, to monitor promoter activity, to allow longer term monitoring
CC   and to localise proteins. (I) has enhanced fluorescence and reduced toxicity. This sequence
CC   substantially enhanced fluorescence and reduced toxicity. (I)
CC   encodes GreenI, a mutant of the wild type green fluorescent protein
CC   isolated from great star coral.
XX
SQ   Sequence 684 BP; 211 A; 138 C; 176 G; 159 T; 0 U; 0 Other;

Query Match   58.8%; Score 626.4; DB 12; Length 684;
Best Local Similarity   94.7%; Pred. No. 2e-179;
Matches 648; Conservative   0; Mismatches 36; Indels   0; Gaps   0;

```
Qy  102 AAGGGTGGTGATTAAACCAGACATGAGAGATGAAGCTGCGTATGGAAGGTGCTGTAAACCGG 161
        ||||||  |||||| |||||||||| ||||| ||||| |||||||||||||||||||||||||
Db    1  ATGAGTGTGATAAAACCAGACACATGAGGAGATCAAGCTGCGTATGGAAGGTGCTGTAAACCGGG 60

Qy  162 CACAAGTTCGTTGGTTGAAGGAGGATGGAAAAGGGAAGCCTTTGAAGGAAGCAGAGACTATG 221
        |||||||||||||| |||||||||||||||||||| ||||||||| ||||| |||||||||||
Db   61 CACAAGTTCGTTGATTGAAGGAGGATGGAAAAGGCAAGCCTTTCGAGGGAAAACAGAGACTATG 120

Qy  222 GACCTTACAGTCATAGAAGGCGCACCATTGCCTTTCGCTTACGATATCTTGACAACAGTA 281
        |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db  121 GACCTTACAGTCATAGAAGGCGCACCTTTGCCTTTCGCTTACGATATCTTGACAACAGTA 180

Qy  282 TTCGATTACGGCCAACGGGTATTCGCCAAATACCCAGAAGAACATAGCAGATTATTCAAG 341
        ||||||||||||||||  |||||||||||||||||| |||||||||||  ||| |||||||
Db  181 TTCGATTACGGCCAACAGGGTATTCGCCAAATACCCAAAAGAACATACCAGACTATTCAAG 240

Qy  342 CAGACGTTCCTGGGACTTCCTGGGACGTACTCCTGGGAACGAAGCATT 401
        ||||||||||  |||||||||||  ||||||||||||||||||||||||
Db  241 CAGACGTTCCGGAGGGGTACTCCTGGGACGAAGCATT 300

Qy  402 TGCATCGCCACAAACGACATAACAATGATGGAAGGCGTCGACGACTGTTTTGCCTATAAA 461
        ||||||||||||||||||||||||||||||| ||||||||||||||||||| ||||||||
Db  301 TGCATCGCCACAAACGACATAACAATGATGAAAGGCGTCGACGACTGTTTTGTCTATAAA 360

Qy  462 ATTGGATTTGATGGTGTGAACTTTCCTGCCAATGTGTCCAGTTATGCAGAGGAAGACGCTG 521
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db  361 ATTGGATTTGATGGTGTGAACTTTCCTGCCAATGTGTCCAGTTATGCAGAGGAAGACGCTA 420

Qy  522 AAATGGGAGCCATCCACTGAGATAATGTATGCGCGTGATGGAGTGCTGAAGGGTGATGTT 581
        |||||||||||||||||||||||||||||||| ||||||||||| |||||||||||||||
Db  421 AAATGGGAGCCATCCACTGAGATAATGTATGCGGGTGATGGAGTGGTGAAGGGTGATGTT 480

Qy  582 AACATGGCTCGTTGCTTGAAGGAGGTGGCCATTACCGATGTGACTTCAAAACTACTTAC 641
        |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db  481 AACATGGCTCGTTGCTTGAAGGAGGTGGCCATTACCGATGTGACTCCAAAACTACTTAC 540

Qy  642 AAAGCTAAGAAGGTTGTCCGGTTGCCGGTGCCAGACTATCACTTTGTGGACCATCCCATTGAGATT 701
        ||||||||||||||||||| |||||| |||||||||| ||||| |||||||| ||||||||
Db  541 AAAGCTAAGAAGGTTGTCCAGTTGCCAGACTATCATTTTGTTGACCATCGCATTGAGATT 600

Qy  702 GTGAGCCACGACAAAGATTACACAAGGTTAAGCTGCCACGAGCATGCCGAAGCTCGTCAT 761
        |||||||||||||||||||||||||||||||||||  | |||||||||||||||||  |
Db  601 GTGAGCCACGACAAAGATTACACAAGGTTAAGCTGTATGAGCATGCCGAAGCTCATTCT 660

Qy  762 GGACTGTCAAGAAGGCCAAGTAA 785
        ||| || |||||||||||
Db  661 GGGCTGCCGAGGCAGGCCAAGTAA 684
```

RESULT 8
AD284226
ID   AD284226 standard; DNA; 684 BP.
XX
AC   AD284226;
XX
DT   14-JUL-2005 (first entry)
XX
DE   Montastraea cavernosa GFP mutant Green I-encoding DNA, SEQ ID NO:5.
XX
KW   Green fluorescent protein; Green I; mutant; gene; ds.
XX
OS   Montastraea cavernosa.
OS   Synthetic.
XX
FH   Key   Location/Qualifiers
FT   CDS   1..684
FT   /tag= a
FT   /product= "Mutant GFP Green I"
FT   mutation   replace(527,T)
FT   /tag= b
FT   /note= "This nucleotide is T in the Green II mutant,
FT   resulting in Phe rather than Ser at position 176 of the
FT   protein"
XX
PN   US2005100954-A1.
XX
PD   12-MAY-2005.
XX
PF   23-DEC-2004; 2004US-00021014.
PR   09-DEC-2002; 2002US-00314936.
XX
PA   (GIBB/) GIBBS P D L.
PA   (CART/) CARTER R W.
PA   (SCHM/) SCHMALE M C.
XX
PI   Gibbs PDL, Carter RW,   Schmale MC;
XX
DR   WPI; 2005-345399/35.
DR   P-PSDB; AD284227.
XX
PT   Novel mutant fluorescent protein comprising amino acid sequence that
PT   differs from wild-type red or green fluorescent protein by amino acid
PT   substitutions, useful as markers for detecting desired gene expression.
XX
PS   Claim 10; SEQ ID NO 5; 29pp; English.
XX
CC   The invention relates to mutant red and green fluorescent proteins which
CC   have higher fluorescent intensities compared to the wild-type proteins
CC   from which they are derived. The invention also discloses nucleic acids
CC   encoding the mutant fluorescent proteins, and transgenic animals
CC   comprising such a nucleic acid. The mutant red fluorescent proteins (RFP)
CC   of the invention, Red I (AD284223) and Red II (AD284225), are derived
CC   from a novel wild-type RFP (referred to as Ac/DsRFP) isolated from a
CC   mushroom coral believed to be either an Actinodiscus or Discosoma
CC   species, while the mutant green fluorescent proteins (GFP), Green I
CC   (AD284227) and Green (AD284229), are derived from a novel wild-type GFP
CC   (known as McGFP) isolated from the great star coral Montastraea
CC   cavernosa. The Ac/DsRFP and McGFP mutants were obtained by subjecting the
CC   wild-type Ac/DsRFP and McGFP cDNAs to low-stringency PCR to introduce
CC   random mutations, cloning the PCR products into bacterial expression
CC   vectors, and selecting the transformed bacteria having higher relative
CC   fluorescence compared to those expressing the wild-type proteins. The
CC   mutant fluorescent proteins of the invention may be used in a wide range
CC   of applications. They are useful as markers for detecting the expression
CC   of a gene of interest, or can be used as in vivo markers in mRNA
CC   microinjection assays in transgenic animals. They can be used in
CC   expression systems (e.g., as components of fusion proteins), in multiple
CC   labeling systems, or can be used in biochemical assays and as reagents.
CC   They may additionally be used as taxonomic markers for studies of
CC   cnidarian genetics, as color indicators in diagnostic kits, as colored
CC   food additives and as cosmetic ingredients. The present sequence

CC   represents DNA encoding the mutant Montastraea cavernosa green
CC   fluorescent protein Green I.
XX
SQ   Sequence 684 BP; 211 A; 138 C; 176 G; 159 T; 0 U; 0 Other;

Query Match   58.8%; Score 626.4; DB 14; Length 684;
Best Local Similarity   94.7%; Pred. No. 2e-179;
Matches 648; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

Qy   102 AAGGGTGTGATTAAACCAGACATGAAGATGAAGCTGCGTATGGAAGGTGCTGAAACGCGG 161
                   |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGAGTGTGATAAAACCAGACATGAAGATCAAGCTGCGTATGGAAGGTGCTGAAACGGG 60

Qy   162 CACAAGTTCGTGGTTGAAGGAGGAGATGGAAAAAGGGAAAAGGCCTTTGACGAACACAGTA 221
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 CACAAGTTCGTGATTGAAGGAGGACGGAAAAAGGCAAGGCCTTTCGACGAACAGAGTA 120

Qy   222 GACCTTACAGTCATAGAAGGGCCACCATTGCCTTCGCTTACGATATCTTGACAACAGTA 281
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GACCTTACAGTCATAGAAGGGCCACCTTTGCCTTTCGCTTACGATATCTTGACAACAGTA 180

Qy   282 TTCGATTACGGCAACAGGGTATTCGCCAAATACCCAGAAGACATAGACATATTTCAAG 341
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TTCGATTACGGCAACAGGGTATTCGCCAAATACCCAAAGACATACCAGACTATTTCAAG 240

Qy   342 CAGACGTTTCCTGAGGGGTACTTCTGGGAACGAAGCATGACATACGAAGAACCAGGGCATT 401
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 CAGACGTTTCCGGAGGGGTACTTCCTCGGGAACGAAGCATGACATACGAAGAACCAGGGCATT 300

Qy   402 TGCATCGCCACAAAGACATAACAATGATGAGAGGCGTCGACGACTGTTTGCCTATAAA 461
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 TGCATCGCCACAAAGACAACAACAATGATGAGAAGGGCGTCGACGACTGTTTGTCTATAAA 360

Qy   462 ATTCGATTTGATGGTGTGAACTTCCTGCCAATGGTCCAGTTATGCAGAGGAAGACGCTG 521
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 ATTCGATTTGATGGTGTGAACTTCCTGCCAATGGTCCAGTTATGCAGAGGAAGACGCTA 420

Qy   522 AAATGGGAGCCATCCACTGAGATAATGTATGCGCGTGATGGTGCTGAAGGGTGATGTT 581
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 AAATGGGAGCCATCCACTGCAAAAAATGTATGTCGGTGATGGTGCTGAAGGGTGATGTT 480

Qy   582 AACATGGCTCGTTGCTTGAAGGAGGTGGCCATTACCGATGTGACTTCAAAACTACTTAC 641
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 AACATGGCTCGTTGCTTGAAGGAGGTGGCCATTACCGATGTGACTCCAAAACTACTTAC 540

Qy   642 AAAGCTAAGAAGGTGTCCGGTTGCCAGACTATCACTTTGTGGACCATCGCATTGAGATT 701
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 AAAGCTAAGAAGGTGTCCCAGTTGCCAGACTATCATTTTGTTGCCATCGCATTGAGATT 600

Qy   702 GTGAGCCACGACAAAGATTACAACAAGGTTAAGCTGCGACGAGCATGCCGAAGTCGTCAT 761
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GTGAGCCACCACGACAAAGATTACAACAAGGTTAAGCTGTGATGAGCATGCCGAAGCTCATTCT 660

Qy   762 GGACTGTCAAGGAGGCCAAGTAA 785
               ||| |||||||||||||||||||
Db   661 GGGCTGCCGAGGCAGGCCAAGTAA 684

RESULT 9
ADW43033
ID   ADW43033 standard; DNA; 684 BP.
XX
AC   ADW43033;
XX
DT   24-MAR-2005 (first entry)
XX
DE   Favia favus fluorescence-related KKH DNA - SEQ ID 13.
XX
KW   fluorescence; protein localization; cellular transport; ss; gene.
XX
OS   Favia favus.
XX
FH   Key   Location/Qualifiers

```
PT    CDS            1..684
PT                   /tag= a
PT                   /product= "Favia favus fluorescence-related KGH protein -
PT                   SEQ ID 12"
XX
PN    WO2004111236-A1.
XX
PD    23-DEC-2004.
XX
PF    16-JUN-2004; 2004WO-JP008790.
XX
PR    16-JUN-2003; 2003JP-00170330.
XX
PA    (RIKE ) RIKEN KK.
PA    (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD.
XX
PI    Miyawaki A, Tsutsui H, Karasawa S;
XX
DR    WPI; 2005-066240/07.
DR    P-PSDB; ADW43032.
XX
PT    Novel fluorescent protein derived from Favia favus, exhibiting specific
PT    excitation maximum wavelength and molar extinction coefficient, useful in
PT    molecular-biological analysis.
XX
PS    Claim 11; SEQ ID NO 13; 66pp; Japanese.
XX
CC    The invention relates to a novel fluorescent protein derived from Favia
CC    favus, exhibiting an excitation maximum wavelength of 507 nm and
CC    fluorescence maximum wavelength of 517 nm, with molar extinction
CC    coefficient of 80000 at 482 nm, quantum yield of 0.68 and pH sensitivity
CC    of fluorescence maximum being stable at pH 5-11. The protein has a fully
CC    defined sequence of SEQ ID NO:1 as given in the specification. The
CC    fluorescent fusion protein of the invention may be useful for analyzing
CC    the location or transport of a protein inside the cell. The current
CC    sequence is that of the Favia favus fluorescence-related KKH DNA (SEQ ID
CC    13) of the invention.
XX
SQ    Sequence 684 BP; 205 A; 131 C; 181 G; 167 T; 0 U; 0 Other;

Query Match         50.7%;  Score 540;  DB 14;  Length 684;
Best Local Similarity   86.8%;  Pred. No. 3.6e-153;
Matches  594;  Conservative   0;  Mismatches  90;  Indels   0;  Gaps   0;

Qy  102 AAGGGTGTGATTAAACCAGACATGAAGATGAAGATGAAGCTGCGTATGGAAGGTGCTGTAAACCGGG 161
        | |||||||||| |||||||||  |||||  ||||||| |||||| ||| ||||||||||||||||
Db    1 ATGAGTGTGATTACATCAGAAATGAAGATGAAGATGAGCTGCGTATGCGGAAGGCTGTAAACCGGG 60

Qy  162 CACAAGTTCGTGGTTGAAGGAGATGGAAAAGGAAAGCCTTTCGACGGAACACAGACTATG 221
        |||||||||||| |||||||||| ||||||||||| ||||||| ||||||||| ||||||
Db   61 CACAAGTTCGTGATTACAGGAGAAGGAAAAGGAAAGGTGGCCAGCCTTTCGAGGGAATACAGAATATG 120

Qy  222 GACCTTACAGTCATAGAGAGGCCGCACCATTGCCTTCGCCTTAGCATATCTTGACAACAGTA 281
        ||||| |||||| ||||||||| ||||  |||| |||||  |||  |||| ||||||||||
Db  121 GACCTGACAGTCAGTCATAGAGAGGGGCCGACCTTCTTCCTTTGCTTTTGCTTTCGATATCCTGACAACAGTA 180

Qy  282 TTCGATTACGGCAACACAGGGTATTCGCCAAATACCCAGAAGACATAGCAGATTATTTCAAG 341
        ||| ||||||||||||  |||||||  |||||||||||||||| |||  ||| ||| |||||
Db  181 TTCCATTACGGCAACCGCGGGTATTTGTCAAATACCCAGAAGAATAGTAGACTACTTCAAG 240

Qy  342 CAGACGTTTCCTGAGGGGTACTTCTGGGAACGAAGCATGACAAGCATGAGTTACGAAGACGAGGCCATT 401
        ||| ||||||||||||||| ||||| |||||||||||||| ||||||||||||||||||| || ||||
Db  241 CAGTCGTTTCCTGAGGGGTTATTCTTGGGAACGAAGCATGAGTTACGAAGACGCGGGGAATT 300

Qy  402 TGCATCGCCACAAACGACACATAACATGATGAAGGGCGTCGACGACTGTTTTGCCTATAAA 461
        ||| | ||| ||||||  ||| ||| |||||||| || | |||  ||||||||| ||| ||
Db  301 TGCCTGCCGCCACAAACAATATAACGATGAAGAGAAGACGGCAGCCAACTGTTTTGTCTCATGAA 360

Qy  462 ATTCGATTTGATGGTGTGAACTTCCTGCCAATGTCCAGTTATGCAGAGAAGACGCTG 521
        |||||||||||||||||||||||||||||||||||||||||||||||||  || || 
Db  361 ATTCGATTTGATGGTGTGAACTTCCTGCCAATGTCCAGTTATGCAGAGAGAAGAAGACCGTC 420

Qy  522 AAATGGGAGCCATCCACTGAGATAATGTATGCGGTGACTGAAGGGTGATGTT 581
        |||||||||||||||||||||  |||||||| |||| ||| |||||||||||
Db  421 AAATGGGAGCCATCCACTGAGAAAATGTATGTGCGTGATGGAGTTGCTGAAGGGTGATGTT 480

Qy  582 AACATGGCTCGTGTTGCTTGAAGGAGTGGCCATTACCGATGTGACTTCAAAACTACTTAC 641
        ||||||||||||||||||||| ||||||||||||||||||||||||||| |||||||||
Db  481 AACATGGCTCGTGTTGCTTGCAAGGAGTGGCCATTACCGATGTGACTTCAGAACTACTTAC 540

Qy  642 AAAGCTAAGAAGGTTGTCCGGTTGCCAGACTATCACTTTGTGGACCATGCCATTGAGATT 701
        || || |||||||||||||  |||||||||||||||||| ||||| |||  |||||||
Db  541 AAGCAAGAAGGTTGTCCAGTTGCCAGACTATCACTTCGTGGATCATGAATTGAGATA 600

Qy  702 GTGAGCCACGACAAAGATTACACAACAAGGTTAAGCTGCACGACGAGCAGCATGCCCAAGTCGTCAT 761
        ||||| || |||||||||||||| |||||||||||||| ||| ||||||| |||| |||||| ||
Db  601 ACAAGCCATGACAAGGATTACAACAAGGTTAAGCTGTATGAGCATGCTAAAGTCATTCC 660

Qy  762 GGACTGTCAAGGAAGGCCAAGTAA 785
        || ||| ||||| || ||||||||
Db  661 GGGCTGCCAAGGCTGGCCAAGTAA 684

RESULT 10
ADW43022
ID   ADW43022 standard; cDNA; 684 BP.
XX
AC   ADW43022;
XX
DT   24-MAR-2005  (first entry)
XX
DE   Favia favus fluorescence-related cDNA - SEQ ID 2.
XX
KW   fluorescence; protein localization; cellular transport; ss; gene.
XX
OS   Favia favus.
XX
FH   Key            Location/Qualifiers
FT   CDS            1..684
FT                  /tag= a
FT                  /product= "Favia favus fluorescence-related protein - SEQ
FT                  ID 1"
XX
PN   WO2004111236-A1.
XX
PD   23-DEC-2004.
XX
PF   16-JUN-2004; 2004WO-JP008790.
XX
PR   16-JUN-2003; 2003JP-00170330.
XX
PA   (RIKE ) RIKEN KK.
PA   (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD.
XX
PI   Miyawaki A, Tsutsui H, Karasawa S;
XX
DR   WPI; 2005-066240/07.
DR   P-PSDB; ADW43021.
XX
PT   Novel fluorescent protein derived from Favia favus, exhibiting specific
PT   excitation maximum wavelength and molar extinction coefficient, useful in
PT   molecular-biological analysis.
XX
PS   Claim 10; SEQ ID NO 2; 66pp; Japanese.
XX
CC   The invention relates to a novel fluorescent protein derived from Favia
CC   favus, exhibiting an excitation maximum wavelength of 507 nm and
CC   fluorescence maximum wavelength of 517 nm, with molar extinction
CC   coefficient of 80000 at 482 nm, quantum yield of 0.68 and pH sensitivity
CC   of fluorescence maximum being stable at pH 5-11. The protein has a fully
CC   defined sequence of SEQ ID NO:1 as given in the specification. The
CC   fluorescent fusion protein of the invention may be useful for analyzing
CC   the location or transport of a protein inside the cell. The fluorescent
CC   protein does not exhibit toxicity in a mammalian cell. The current
CC   sequence is that of the Favia favus fluorescence-related cDNA (SEQ ID 2)
```

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FT      /tag= a
FT      /product= "Favia favus fluorescence-related H8PV protein
FT       - SEQ ID 14"
XX
PN      WO2004111236-A1.
XX
PD      23-DEC-2004.
XX
PF      16-JUN-2004; 2004WO-JP008790.
XX
PR      16-JUN-2003; 2003JP-00170330.
XX
PA      (RIKE ) RIKEN KK.
PA      (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD.
XX
PI      Miyawaki A, Tsutsui H, Karasawa S;
XX
DR      WPI; 2005-066240/07.
DR      P-PSDB; ADW43034.
XX
PT      Novel fluorescent protein derived from Favia favus, exhibiting specific
PT      excitation maximum wavelength and molar extinction coefficient, useful in
PT      molecular-biological analysis.
XX
PS      Claim 11; SEQ ID NO 15; 66pp; Japanese.
XX
CC      The invention relates to a novel fluorescent protein derived from Favia
CC      favus, exhibiting an excitation maximum wavelength of 507 nm and
CC      fluorescence maximum wavelength of 517 nm, with molar extinction
CC      coefficient of 80000 at 482 nm, quantum yield of 0.68 and pH sensitivity
CC      of fluorescence maximum being stable at pH 5-11. The protein has a fully
CC      defined sequence of SEQ ID NO:1 as given in the specification. The
CC      fluorescent fusion protein of the invention may be useful for analyzing
CC      the location or transport of a protein inside the cell. The fluorescent
CC      protein does not exhibit toxicity in a mammalian cell. The current
CC      sequence is that of the Favia favus fluorescence-related H8PV DNA (SEQ ID
CC      15) of the invention.
XX
SQ      Sequence 684 BP; 204 A; 131 C; 183 G; 166 T; 0 U; 0 Other;
```

```
Query Match             50.4%;  Score 536.8;  DB 14;  Length 684;
Best Local Similarity   86.5%;  Pred. No. 3.4e-152;
Matches   592;  Conservative    0;  Mismatches   92;  Indels    0;  Gaps    0;

Qy        102 AAGGGTGTGATTAAACCAGACATGAAGATGAAGATGAGAAGAGAAGCTGGTATGGAAGCTGTGTAAACGGG 161
                | |||||||||||||||| |||||||| ||||||||||||||||||||| ||||||||||||||||||||
Db          1 ATGAGTGTGATTACATCAGAAATGAAGATGAGAAGAGAAGCTGGTATGGAAGCGCTGTAAACGGG 60

Qy        162 CACAAGTTCGTGGTTGAAGGAGCCTTTCGACGAACCAGACTATG 221
                ||||||||||||||| ||||  ||||||||| ||||||||||||
Db         61 CACAAGTTCGTGATTACAGGGAAGAAGAAGTGGCCAGCCTTTCGAGGGAATACAGAAGTG 120

Qy        222 GACCTTACAGTCATAGAAGGCGCACCATTGCCTTCGCTTACGATATCTTGACAACAGTA 281
                ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        121 GACCTGACAGTCATAGAGGGGGACCTCTTCCTTTGCTTTCGATATCCTGACAACAGTA 180

Qy        282 TTCGATTACGGCAACAGGTATTCGCCAAATACCCAGAAGACATAGCAGATTATTCAAG 341
                |||||||||||||| |||||||| |||||||||||||||||||| || ||||||||||
Db        181 TTCGATTACGGCAACCGGTATTTGTCAAATACCCAGAAGAAATAGTAGACTACTTCAAG 240

Qy        342 CAGACGTTTCCTGAGGGTACTTCTGGAACGAAGCATGACATACGAAGACCAGGGCATT 401
                ||||||||||||| ||| ||||||||||||| ||||||||||||||||||||||||
Db        241 CAGTCGTTTCCTGAGGGTTATTCTTGGGAACCAGAAGCATGAGTTACGAAGACGGGGGAATT 300

Qy        402 TGCATCGCCACAAACGACATAACAATGATGAAGCGTCGACGACTGTTTTCGACGGCAACACAGACTATG 461
                || |||||||||| |||||||| ||||||||| || |||||  | ||||||| |||| |||||||||||||
Db        301 TGCCTCGCCACAAACAATATAACGATGAAAAGAACGGCAGCAACTGTTTTGTCTCATGAA 360

Qy        462 ATTCGATTTGATGGTGTGAACTTCTGCGTCCAGTTATGCGAGGAAGACGCTG 521
                |||||||| ||||||||||||||||||| |||||||| || ||||||||||||
Db        361 ATTCGATTTGATGGTGTGAACTTTGCCAATGGTCCAGTTATGCGAGGAAGACCGTC 420

Qy        522 AAATGGGAGCCATCCACTGAGATAATGTATCGCGTGATGAGTGCTGAAGGGTGATGTT 581
```

CC   21) of the invention.
XX
SQ   Sequence 684 BP; 203 A; 133 C; 183 G; 165 T; 0 U; 0 Other;

Query Match   50.1%; Score 533.6; DB 14; Length 684;
Best Local Similarity 86.3%; Pred. No. 3.2e-151;
Matches 590; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

```
Qy    102 AAGGGTGTGATTAACCAGACATGAAGATGAAGATGAAGGTGCTATGAAACGGG 161
          ||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db      1 ATGAGTGTGATTACATCAGAAAATGAAGATGAAGATGGAGCTGGCGCTGTAAACGGG 60

Qy    162 CACAAGTTCGTGGTTGAAGGAGATGGAAAAGGAAAAGGCCTTCGACGGAACCAGACTATG 221
          ||||||||||||||||  ||| ||  ||||||||| |||||||||||||||||||||||||
Db     61 CACAAGTTCGTGATTACAGGGAAAGGAAGAGGTGGCCAGCCTTCGAGGGAATACAGAATATG 120

Qy    222 GACCTTACGTCATAGAAGGCGCCACCATTCGCCTTCGCTTACGATATCTTGACAACAGTA 281
          ||||   |||| |||| ||  ||||| || ||||| ||||| | ||||||||||||||||
Db    121 GACCTGACAGTCATAGAGCGGGCCACCATCCCTTTCGATATCCTGCAGAACAGCA 180

Qy    282 TTCGATTACGGCAACACAGGGTATTCGCCAAAATACCCAGAAGACATAGCAGATTATTTCAAG 341
          ||||||||||||||||||||| || || ||||| ||||||||||||||| || ||||||||||
Db    181 TTCGGTCACGGCAACCGGGTATTTGTCAAATACCCAGAAGAAATAGTAGACTACTTCAAG 240

Qy    342 CAGACGTTTCCTGAGGGTACTTCTGGGAACGAAGCATGAAGCATACGAAGACCAGGGCATT 401
          ||||||||||||||||||  || || ||||| |||||||||||| ||||||||| |||||||
Db    241 CAGTCGTTTCCTGAGGGTTATTCTTGGGAACGAAGCATGAGTTACGAAGACGGGGGAATT 300

Qy    402 TGCATGCCACAAACGACATAACAATGATGGAAGGGCTGCGACGACTGTTTGCCTATAAA 461
          ||||||| ||||||||| ||||| |||| ||||||| ||||| |||||||||||| |||||
Db    301 TGCCTCGCCACAAACAATATATAACGATGAAGAAGAAGACGGCAGCAACTGTTTTGTCTATGAA 360

Qy    462 ATTCGATTTGATGGTGTGAACTTCTGCTGCCAATGGTCCAGTTATGCAGAGGAAGACGCGTG 521
          ||||||||||||||||||||||||||| ||||||||||||||| |||| |||||||| ||
Db    361 ATTCGATTTGATGGTGTGAACTTCTGCTGCCAATGGTCCAGTTATGCAGAGGAAGAACGACCGTC 420

Qy    522 AAATGGGAGCCATCCACTCCTGCGTGAGATAATGTATGCGCGTGATGGAGTGCTGAAGGGTGATGTT 581
          ||||||||||||||||||||| |||||||| |||||||||| |||||||| ||||||||||||||||
Db    421 AAATGGGAGCCATCCACTCCTGCGTGAGAAAATGTATGCGTGATGGAGTGCTGAAGGGTGATGTT 480

Qy    582 AACATGGCTCGTGTTGCTTGAAGGAGGTGGCCATTACCGATGTGAACTTCAAAACTACTTAC 641
          |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db    481 AACATGGCTCGTGTTGCTTGCTTCAAGGAGGTGGCCATTACCGATGTGACTTCAGAACTACTTAC 540

Qy    642 AAAGCTAAGAAGGTTGTCCGGTTGCCAGACTATCACTTTGTGGACCATCGCATTGAGATT 701
          |||||||||||||||| ||||||||||||||||||||||||||| |||||||||||||||
Db    541 AAAGCAAGAAGGTTGTCCAGTTGCCAGACTATCACTTTGTGGATCTTCGAACTGAGATA 600

Qy    702 GTGAGCCACGACAAAGATTACAACAAGGTTAAGCTGCACGAGCATGCCGAAGCTCGTCAT 761
          |||||||||||||||| ||||||||||||||||| || ||||||||||| |||||||||
Db    601 ACAAGCCATGACACAAGGATTACAACAAGGTTAAGCTGTATGAGCATGTGTAAAGCTCATTCC 660

Qy    762 GGACTGTCAAGGAAGGCCAAGTAA 785
          || |||||||||||||||||||||
Db    661 GGGCTGCCAAGGCTGGCCAAGTAA 684
```

RESULT 13
AAL60080
ID AAL60080   standard; DNA; 795 BP.
XX
AC AAL60080;
XX
DT 27-AUG-2003 (first entry)
XX
DE Montastraea cavernosa red fluorescent protein (mcavRFP) encoding DNA.
XX
KW Chromoprotein; fluorescent protein; colouring agent; food composition;
KW cosmetic; fluorescence resonance energy transfer; calcium ion indicator;
KW biosensor; pH indicator; phosphorylation indicator; messenger detector;
KW transgenic animal; fluorescent timer; red fluorescent protein; RFP;
KW transgenic; gene; ds.
XX

```
Db    421 AAATGGGAGCCATCCACTCCTGCTTGAAGATAATGTATGCGCGTGATGGAGTGCTGAAGGGTGATGTT 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    582 AACATGGCTCGTGTTGCTTGAAGGAGGTGGCCATTACCGATGTGAACTTCAAAACTACTTAC 641
          |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db    481 AACATGGCTCGTGTTGCTTGCTTCAAGGAGGTGGCCATTACCGATGTGACTTCAGAACTACTTAC 540
Qy    642 AAAGCTAAGAAGGTTGTCCGGTTGCCAGACTATCACTTTGTGGACCATCGCATTGAGATT 701
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 AAAGCAAGAAGGTTGTCCAGTTGCCAGACTATCACTTTGTGGATCTTCGAACTGAGATA 600
Qy    702 GTGAGCCACGACAAAGATTACAACAAGGTTAAGCTGCACGAGCATGCCGAAGCTCGTCAT 761
          ||||||||||||||||||||||||||||||||||||||||||
Db    601 ACAAGCCATGACACAAGGATTACAACAAGGTTAAGCTGTATGAGCATGTGTAAAGCTCATTCC 660
Qy    762 GGACTGTCAAGGAAGGCCAAGTAA 785
          |||||||||||||||||||
Db    661 GGGCTGCCAAGGCTGGCCAAGTAA 684
```

RESULT 12
ADW43041
ID ADW43041   standard; DNA; 684 BP.
XX
AC ADW43041;
XX
DT 24-MAR-2005 (first entry)
XX
DE Favia favus fluorescence-related KBL2 DNA - SEQ ID 21.
XX
KW fluorescence; protein localization; cellular transport; ds; gene.
OS Favia favus.
XX
FH Key   Location/Qualifiers
FT CDS   1..684
FT   /tag= a
FT   /product= "Favia favus fluorescence-related KBL2 protein
FT   - SEQ ID 21"
FT   /transl_except= (pos:280. .282, aa:Xaa)
XX
PN WO2004111236-A1.
XX
PD 23-DEC-2004.
XX
PF 16-JUN-2004; 2004WO-JP008790.
XX
PR 16-JUN-2003; 2003JP-00170330.
XX
PA (RIKE) RIKEN KK.
PA (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD.
XX
PI Miyawaki A, Tsutsui H, Karasawa S;
XX
DR WPI; 2005-066240/07.
DR P-PSDB; ADW43040.
XX
PT Novel fluorescent protein derived from Favia favus, exhibiting specific
PT excitation maximum wavelength and molar extinction coefficient, useful in
PT molecular-biological analysis.
XX
PS Claim 11; SEQ ID NO 21; 66pp; Japanese.
XX
CC The invention relates to a novel fluorescent protein derived from Favia
CC favus, exhibiting an excitation maximum wavelength of 507 nm and
CC fluorescence maximum wavelength of 517 nm, with molar extinction
CC coefficient of 80000 at 482 nm, quantum yield of 0.68 and pH sensitivity
CC of fluorescence maximum being stable at pH 5-11. The protein has a fully
CC defined sequence of SEQ ID NO:1 as given in the specification. The
CC fluorescent fusion protein of the invention may be useful for analyzing
CC the location or transport of a protein inside the cell. The fluorescent
CC protein does not exhibit toxicity in a mammalian cell. The current
CC sequence is that of the Favia favus fluorescence-related KBL2 DNA (SEQ ID

```
Qy    298  GGGTATTCGCCAAATACCCAGAAGACATAGCAGATTATTTCAAGCAGACGTTTCCTGAGG  357
           ||||||||||||||||||||||||||||||  ||||||| ||||||||||||||||||||
Db    288  GGGTATTCGCCAAATACCCAAAACATATCCCAGACTATTTCAAGCAGATGTTTCCTGAGG  347

Qy    358  GGTACTTCTCGGGAACGAGCATGACATACGAAGACCAGGGCATTTGCATCGCCACAAACG  417
           |||| |||||||||||||| ||||||| |||||||||||||||||||||||| |||| ||
Db    348  AGTATTCCTGGGAACGAAGCATGAATTTCGAAGGCGGGGGCATTTGCACCCGCCAGGAACG  407

Qy    418  ACATAACAATGATGGAAGGCGTCGACGACTGTTTGCCTATAAAATTCGATTTGATGGTG  477
           ||||||                          |||||||||||| ||||||||||||||
Db    408  AGATAACAATG---------GAAGGCGACTGTTTTTCAATAAAGTTCGATTTGATGGTG  458

Qy    478  TGAACTTTCTGCCAATGGTCCAGTTATGCAGAGAGAACGCTGAAATGGGAGCCATCCA  537
           ||||||||| |||||||||||||||||| ||||||||||||||||| |||||||||||
Db    459  TGAACTTCCCCCATGGTCCAGTCATGCAGAAGAAGAGACGCTGAAATGGGAGCCATCCA  518

Qy    538  CTGAGATAATGTATGCGGTGATGGAGTGCTGAAGGGTGATGTATCAACATGGCTTTGTTGC  597
           ||| |   | || |||||||||||||||||||||| |||||| | |||||||||| |||||
Db    519  CTGAAAAAATGTATGTGCGTGATGGAGTGCTGACGGGTGATGTATCAACATGGCTTTGTTGC  578

Qy    598  TTGAAGGAGGTGGCCATTACCCATGTGACTTCAAAACTACTTACAAAGCT---AAGAAGG  654
           ||||||||||||||||||||||||||||||| |||| ||||||||||| | |||||||||
Db    579  TTGAAGGAGGTGGCCATTACCCATGTGACTTCAGAACTACTTACAGAGCTAAGAAGAAGG  638

Qy    655  TTGTCCGGTTGCCAGACTATCACTTTGTGGACCATCGCATTGAGATTGTGAGCCACGACA  714
           ||||| |||||||||||||| ||||| || |||||| |||||| |||||||| |||||||
Db    639  GTGTCAAGTTACCAGATTATCATTTGAGGATCACTCCATTGAGATTTTGCGCCATGACA  698

Qy    715  AAGATTACAACAAGGTTAAGCTGCCACGAGCTCGTCATGGACTGTCAAGGA  774
           ||||| ||||| ||||||||||||||       |||||||||||||||||||
Db    699  AAGAATACACTGAGGTTAAGCTGTATGAGCATGCCCAAGCTTCATTCTGGGCTGCCGAGGG  758

Qy    775  AGGCCAAGTAAAGCTTAATGAAAGTCAAGACGACA  811
           ||                 |||| ||||||||||| ||
Db    759  TGGCAAGTAAAGGCTTAACGAAAGCCAAGACCACA  795
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RESULT 14
ADW43037
ID ADW43037 standard; DNA; 684 BP.
XX
AC ADW43037;
XX
DT 24-MAR-2005 (first entry)
XX
DE Favia favus fluorescence-related H8PVLM DNA - SEQ ID 17.
XX
KW fluorescence; protein localization; cellular transport; ds; gene.
XX
OS Favia favus.
XX
FH Key   Location/Qualifiers
FT CDS
FT   1..684
FT   /tag= a
FT   /product= "Favia favus fluorescence-related H8PVLM
FT   protein - SEQ ID 16"
XX
PN WO2004111236-A1.
XX
PD 23-DEC-2004.
XX
PF 16-JUN-2004; 2004WO-JP008790.
XX
PR 16-JUN-2003; 2003JP-00170330.
XX
PA (RIKE) RIKEN KK.
PA (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD.
XX
PI Miyawaki A, Tsutsui H, Karasawa S;
XX
DR WPI; 2005-066240/07.
DR P-PSDB; ADW43036.

OS Montastraea cavernosa.
XX
FH Key   Location/Qualifiers
FT CDS
FT   62..769
FT   /tag= a
FT   /product= "mcavRFP protein"
FT   /note= "No start codon"
FT   /partial
XX
PN WO200304240L-A2.
XX
PD 22-MAY-2003.
XX
PF 12-NOV-2002; 2002WO-US036499.
PR 13-NOV-2001; 2001US-0332980P.
XX
PA (CLON-) CLONTECH LAB INC.
XX
PI Labas YA, Gurskaya NG, Yanushevich Y, Fradkov AF, Lukyanov K;
PI Lukyanov S, Matz MV;
XX
DR WPI; 2003-482353/45.
DR P-PSDB; AAO29585.
XX
PT New chromo and/or fluorescent-protein encoding nucleic acids, the
PT proteins being useful as labels in analyte detection assays, as
PT selectable markers in recombinant DNA application, or as biosensors in
PT prokaryotic and eukaryotic cells.
XX
CC Claim 1; Fig 15; 88pp; English.
XX
CC The invention relates to novel chromo and/or fluorescent proteins and
CC nucleic acid molecules encoding such proteins. Sequences of the invention
CC are useful as labelling tools for marking a protein, cell or organism in
CC biochemistry, molecular biology and medical diagnostic applications.
CC Chromoproteins are useful as colouring agents capable of imparting colour
CC or pigment to a particular composition of matter, e.g. food compositions,
CC pharmaceuticals or cosmetics, as labels in analyte detection assays, or
CC as selectable markers in recombinant DNA applications. Fluorescent
CC proteins are useful in fluorescence resonance energy transfer
CC applications, in high-throughput screening assays, as biosensors in
CC prokaryotic and eukaryotic cells e.g. as calcium ion indicator, as pH
CC indicator or as phosphorylation indicator, as second messenger detectors,
CC as in vivo markers in transgenic animals, or as fluorescent timers. The
CC present sequence is Montastraea cavernosa red fluorescent protein
CC (mcavRFP) encoding DNA
XX
SQ Sequence 795 BP; 246 A; 159 C; 205 G; 185 T; 0 U; 0 Other;

Query Match   50.0%; Score 533.4; DB 8; Length 795;
Best Local Similarity   83.2%; Pred. No. 4e-151;
Matches 680; Conservative   0; Mismatches 101; Indels 36; Gaps 5;

```
Qy    1    ATTCGCCCTGCGTGATTTGGAAGAGCAGATCGAGAACAACAAGAGCTG--TAAGGTTGA  58
           |||||||||||||||||||||||||||||||||||||||||||||||||  |||||||||
Db    9    ATTCACCCTGGGTGATTTGGAAGAGGAGCAGACCGAGAACAACAAGAGCTGTATAAGGCTGA  68

Qy    59   TATCTTAC-TTACGTCTACCATCATGACAAGTGTTGCACAGGAAAAGGGTGTGATTAAAC  117
           ||||||||  ||||||||||||||||||||                |||||||||||||
Db    69   TATCTTACTTTACGTCTACCATGA----------------------GTGTGATTAAAT  107

Qy    118  CAGACATGAAGATGAAGCTGCGTATGGAAGGTCGTAAACGGCACACAAGTTCGTGGTTG  177
           |||||||||||||||||||| |||||||||| ||||||||||||||||||||||||||
Db    108  CAGTCATGAAGATCAAGCTGCGTATGGAAGGCAGCGTAAACGGGCACACTTCGTAATTG  167

Qy    178  AAGGAGGATGGAAAAGGGAAGGGAAGCCTTTCGACGGAACCTTACGACTTACAGTCATAG  237
           |||| |||||  || ||| |||||||||||||||              ||||||||||| ||
Db    168  TTGGAGGAGGATGGAAGGCAAGCCTTATGGGAACCAGAGTATGGACCTTACAGTCAAAG  227

Qy    238  AAGGCGCACCATTGCCTTTCGCTTACGATATCTTGACAACAGTATTCGATTACGGCAACA  297
           |||||||||||||| |||||||||||| ||||| |||||||||  ||||||||||||||
Db    228  AAGGCGACCACCTCTGCCTTTCGCCTACGATATCATCAGTATATCCATTCCATTACGGCAATA  287
```

```
XX
PT   Novel fluorescent protein derived from Favia favus, exhibiting specific
PT   excitation maximum wavelength and molar extinction coefficient, useful in
PT   molecular-biological analysis.
XX
PS   Claim 11; SEQ.ID NO 17; 66pp; Japanese.
XX
CC   The invention relates to a novel fluorescent protein derived from Favia
CC   favus, exhibiting an excitation maximum wavelength of 507 nm and
CC   fluorescence maximum wavelength of 517 nm, with molar extinction
CC   coefficient of 80000 at 482 nm, quantum yield of 0.68 and pH sensitivity
CC   of fluorescence maximum being stable at pH 5-11. The protein has a fully
CC   defined sequence of SEQ ID NO:1 as given in the specification. The
CC   fluorescent fusion protein of the invention may be useful for analyzing
CC   the location or transport of a protein inside the cell. The fluorescent
CC   protein does not exhibit toxicity in a mammalian cell. The current
CC   sequence is that of the Favia favus fluorescence-related H8PVLM DNA (SEQ
CC   ID 17) of the invention.
XX
SQ   Sequence 684 BP; 205 A; 131 C; 182 G; 166 T; 0 U; 0 Other;

Query Match        49.5%;    Score 527.2;   DB 14;   Length 684;
Best Local Similarity   85.7%;     Pred. No. 2.8e-149;
Matches  586;  Conservative   0;   Mismatches  98;   Indels   0;   Gaps   0;

Qy  102 AAGGGTGTGATTAAACCAGACATGAAGATGAAGCTGCCTATGGAAGGTGCTGTAAACGGG 161
            ||||| ||||||||  |||||||| |||||||   ||  ||||||||||| |||||||||||
Db    1 ATGAGTGTGATTACATCAGAAATGAAGATCAGAGTGCGTATGGAAGGCGCTGTAAACGGG 60

Qy  162 CACAAGTTCGTGTTGAAGGAGGAGATGAAAAGGAAGCCTTTCGACGCGAACACAGACTATG 221
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Qy  222 GACCTTACAGTCATAGAGAAGACAGGGTATTCGCCAAATACCCAGAAGACATAGCAGATTATTTCAAG 281
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Qy  282 TTCGATTACGGCAACACAGGTATTCGCCAAATACCCAGAAGACATAGCAGATTATTTCAAG 341
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Qy  342 CAGAGCGTTTCCTGAGGGTACTTCTGGGAACGAAGCATGACATGACGAAGACCAGGGCATT 401
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Qy  402 TGCATCGGCACAAACGACATACAACATGATGGAAGGCGTCGAGACTGTTTTGCCTATAAA 461
            |||  |  |||||||   |  || || |||||||  |  ||||| |||||||||| || ||
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Qy  462 ATTCGATTTGATGGTGTGAACTTTCCTGCCAATGGTCCAGTTATGCAGAGGAAGACGCTG 521
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Qy  582 AACAATGCTCTGTGCTTGAAGGAGGTGGCCATTACCGATGTGACTTCAAAACTACTTAC 641
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Qy  642 AAAGCTTAAGAAGGTTGTCCGGTTGCCAGACTATCACTTTGTGGACCATCGCATTGAGATT 701
            |||||  |||||||||||||  ||||||||||||||||||| ||||  |||  | ||||||
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Qy  702 GTGAGCCACGACAAAGATTACACAACAAGTTAAGCTGACGAGCAGCATGCCGAAGCTCGTCAT 761
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Qy  762 GGACTGTCAAGGAAGGCAAGTAA 785
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Db  661 GGGCTGCCAAGGCTGGCCAAGTAA 684
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RESULT 15
ADW43039
ID   ADW43039 standard; DNA; 684 BP.
XX
AC   ADW43039;
XX
DT   24-MAR-2005  (first entry)
XX
DE   Favia favus fluorescence-related KikGR DNA - SEQ ID 19.
XX
KW   fluorescence; protein localization; cellular transport; ds; gene.
XX
OS   Favia favus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..684
FT                   /tag= a
FT                   /product= "Favia favus fluorescence-related KikGR protein
FT                   - SEQ ID 18"
XX
PN   WO200411236-A1.
XX
PD   23-DEC-2004.
XX
PF   16-JUN-2004; 2004WO-JP008790.
XX
PR   16-JUN-2003; 2003JP-00170330.
XX
PA   (RIKE ) RIKEN KK.
PA   (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD.
XX
PI   Miyawaki A, Tsutsui H, Karasawa S;
XX
DR   WPI; 2005-066240/07.
DR   P-PSDB; ADW43038.
XX
PT   Novel fluorescent protein derived from Favia favus, exhibiting specific
PT   excitation maximum wavelength and molar extinction coefficient, useful in
PT   molecular-biological analysis.
XX
PS   Claim 11; SEQ ID NO 19; 66pp; Japanese.
XX
CC   The invention relates to a novel fluorescent protein derived from Favia
CC   favus, exhibiting an excitation maximum wavelength of 507 nm and
CC   fluorescence maximum wavelength of 517 nm, with molar extinction
CC   coefficient of 80000 at 482 nm, quantum yield of 0.68 and pH sensitivity
CC   of fluorescence maximum being stable at pH 5-11. The protein has a fully
CC   defined sequence of SEQ ID NO:1 as given in the specification. The
CC   fluorescent fusion protein of the invention may be useful for analyzing
CC   the location or transport of a protein inside the cell. The current
CC   protein does not exhibit toxicity in a mammalian cell. The current
CC   sequence is that of the Favia favus fluorescence-related KikGR DNA (SEQ
CC   ID 19) of the invention.
XX
SQ   Sequence 684 BP; 206 A; 133 C; 182 G; 163 T; 0 U; 0 Other;

Query Match        49.5%;    Score 527.2;   DB 14;   Length 684;
Best Local Similarity   85.7%;     Pred. No. 2.8e-149;
Matches  586;  Conservative   0;   Mismatches  98;   Indels   0;   Gaps   0;

Qy  102 AAGGGTGTGATTAAACCAGACATGAAGATGAAGCTGCCTATGGAAGGTGCTGTAAACGGG 161
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Db    1 ATGAGTGTGATTACATCAGAAATGAAGATCAGAGTGCGTATGGAAGGCGCTGTAAACGGG 60

Qy  162 CACAAGTTCGTGTTGAAGGAGGAGATGAAAAGGAAGCCTTTCGACGCGAACACAGACTATG 221
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Qy  222 GACCTTACAGTCATAGAGAAGACAGGGCCACCATTGCCTTCGCTTAGCGATATCTTGACAACAGTA 281
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Db  121 GACCTGACAGTCATAGAGAGGGGCGGACCTCTTCCTTTTGCTTTCGATATCCTGACAACAGCA 180
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Qy    282  TTCGATTACGGCAACAGGGTATTCGCCAAATACCCAGAAGACATAGCAGATTATTTCAAG   341
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Db    181  TTCCATTACGGCAACCCGGGTATTTGTCGAATACCCAGAAGAAATAGTAGACTACTTCAAG   240

Qy    342  CAGACGTTTCCTGAGGGGTACTTCTGGGAACGAAGCATACGAAGATCGAAGACCAGGGCATT   401
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Db    241  CAGTCGTTTCCTGAGGGTTATTCTTGGGAACGAAGCATGAGTTACGAAGACGGGGGAATT   300

Qy    402  TGCATCGCCACAAACGACATAACAATGATGGAAGGCGTCGACGACTGTTTTGCCTATAAA   461
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Db    301  TGCCTCGCCACAAACAATATATACGATGAAGAAAGACGGCAGCAACTGTTTTGTCAATGAA   360

Qy    462  ATTCGATTGATGGTGTGAACTTCCTGCCAATGGTCCAGTTATGCAGAGGAAGACGCTG   521
           |||||||||||||||||||||| |||||||||||||||||||||||||||||||| |
Db    361  ATTCGATTTGATGGTGTGAACTTCCTGCCAATGGTCCAGTTATGCAGAGGAAGACCCGTC   420

Qy    522  AAATGGGAGCCATCCACTGAGATAATGTATGCCGCGTGATGGAGTGCTGAAGGGTGATGTT   581
           |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db    421  AAATGGGAGCCATCCACTGAGAAAATGTATGCCGTGATGGAGTGCTGAAGGGTGATGTA   480

Qy    582  AACATGGCTCTGTTGCTTGAAGGAGGTGGCCATTACCGATGTGACTTCAAAACTACTTAC   641
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Db    481  AACATGGCTCTGTTGCTTCAAGGAGGTGGCCATTACCGATGTGACTTCAGAAACTACTTAC   540

Qy    642  AAAGCTAAGAGAGGTTGTCCGGTTGCCGACTATCACTTTGTGGACCATCGCATTGAGATT   701
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Db    541  AAAGCAAAGAGAGGTTGTCCAGTTGCCGACTATCACTTCGTCGGATCATCAAATGGAGATA   600

Qy    702  GTGAGCCACGACCAAAGATTACAACAAGGTTAAGCTGCACGAGCCATGCCGAAGCTCGTCAT   761
           |||||||||||||| || ||||| | |||||||||||| ||||||| |||  | ||||| |
Db    601  ACAAGCCATGACAAGGTTACAACAACAGGTTAAGCTGTATGAGCATGCTAAAGCTCATTCC   660

Qy    762  GGACTGTCAAGGAAGGCCAAGTAA   785
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Db    661  GGGCTGCCAAGGCTGGCCAAGTAA   684
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Search completed: April 5, 2006, 21:14:38
Job time : 771 secs